

OM of: us-09-680-514-4 to: US09680514.pep:* out_format : pfs
Date: Apr 8, 2002 2:21 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=framet_n2p.model -DEV=xlp -Q=us-09-680-514-4
-DB=US09680514.pep -OUT=align_4.pep.res -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -IOFCL=0.000 -LOPEXT=0.000
-GAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500
-DEPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DEPOP=6.000 -DEEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -ICPU=3 -LONGLOG
-NO_XLPXY -THREADS=1

Search information block:

Query: us-09-680-514-4

Query length: 1047

Database: US09680514.pep:*

Database sequences: 24

Database length: 2736

Search time (sec): 17.370000

score_list:

Sequence	Strd Orig	zScore	EScore	Len	Documentation
US09680514.pep:US-09-680-514-5	1	1769.00	733.73	3.6e-38	349
US09680514.pep:US-09-680-514-7	1	1753.00	727.40	7.8e-38	361
US09680514.pep:US-09-680-514-9	1	1751.00	726.61	8.6e-38	365
US09680514.pep:US-09-680-514-1	1	1677.00	697.37	4.0e-36	328
US09680514.pep:US-09-680-514-2	1	1661.00	691.05	8.8e-36	340
US09680514.pep:US-09-680-514-3	1	1659.00	690.26	9.6e-36	344
US09680514.pep:US-09-680-514-39	1	851.00	371.00	1.1e-17	175
US09680514.pep:US-09-680-514-40	1	835.00	364.67	1.4e-17	332
US09680514.pep:US-09-680-514-2	1	87.50	69.31	0.3672	340
US09680514.pep:US-09-680-514-3	1	87.50	69.31	0.3629	344
US09680514.pep:US-09-680-514-7	1	87.50	69.31	0.3458	361
US09680514.pep:US-09-680-514-9	1	87.50	69.31	0.3420	365
US09680514.pep:US-09-680-514-1	1	82.50	67.34	0.4871	328
US09680514.pep:US-09-680-514-5	1	82.50	67.34	0.4578	349
US09680514.pep:US-09-680-514-40	1	56.00	56.87	1.69	332
US09680514.pep:US-09-680-514-15	1	48.00	0.00	338.75	8
US09680514.pep:US-09-680-514-17	1	48.00	0.00	338.75	8
US09680514.pep:US-09-680-514-39	1	48.00	0.00	338.75	175
US09680514.pep:US-09-680-514-31	1	44.00	0.00	338.75	8
US09680514.pep:US-09-680-514-33	1	42.00	0.00	338.75	8
US09680514.pep:US-09-680-514-28	1	40.00	0.00	338.75	8
US09680514.pep:US-09-680-514-26	1	36.00	0.00	301.11	9
US09680514.pep:US-09-680-514-42	1	34.00	48.17	86.08	16
US09680514.pep:US-09-680-514-35	1	34.00	48.17	81.01	17
US09680514.pep:US-09-680-514-42	1	33.00	47.78	89.09	16
US09680514.pep:US-09-680-514-35	1	33.00	47.78	83.85	17
US09680514.pep:US-09-680-514-44	1	32.00	47.38	132.87	12
US09680514.pep:US-09-680-514-24	1	32.00	47.38	113.42	13
US09680514.pep:US-09-680-514-44	1	30.00	46.59	131.14	12
US09680514.pep:US-09-680-514-24	1	30.00	46.59	121.05	13
US09680514.pep:US-09-680-514-21	1	23.00	0.00	338.75	8
US09680514.pep:US-09-680-514-31	1	23.00	0.00	338.75	8
US09680514.pep:US-09-680-514-33	1	23.00	0.00	338.75	8
US09680514.pep:US-09-680-514-15	1	22.00	0.00	338.75	8
US09680514.pep:US-09-680-514-17	1	22.00	0.00	338.75	8
US09680514.pep:US-09-680-514-45	1	22.00	0.00	338.75	8
US09680514.pep:US-09-680-514-45	1	22.00	0.00	338.75	8
US09680514.pep:US-09-680-514-26	1	22.00	0.00	301.11	9
US09680514.pep:US-09-680-514-19	1	20.00	0.00	338.75	8
US09680514.pep:US-09-680-514-21	1	20.00	0.00	338.75	8
US09680514.pep:US-09-680-514-19	1	18.00	0.00	338.75	8
US09680514.pep:US-09-680-514-28	1	17.00	0.00	338.75	8

seq_name: US09680514.pep:US-09-680-514-5

seq_documentation_block:

; Sequence 5, Application: US/09680514

; GENERAL INFORMATION:

; APPLICANT: Yokoi, Haruhiko

; Shiotsu, Yukimasa

; Konishi, Noboru

; TITLE OF INVENTION: NOVEL POLYPEPTIDES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 North Glebe Rd. 8th floor

; CITY: Arlington

; STATE: VA

; COUNTRY: USA

; ZIP: 22201-4741

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/680,514

; FILING DATE: 06-Oct-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/765,337

; FILING DATE: <Unknown>

; APPLICATION NUMBER: JP P.HEI.7-102625

; FILING DATE: 26-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 249-89

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-816-4000

; TELEFAX: 703-816-4100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 349 amino acids

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-680-514-5

alignment_scores:

Quality: 1769.00 Length: 349

Ratio: 5.069 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

us-09-680-514-4 x us-09-680-514-5

Align seg 1/1 to: US-09-680-514-5 from: 1 to: 349

1 ATGAGCTGACTGAATTCCTCTCGTGGTCATGCTTCTCTCACTGCAAG 50

|||||

1 MetGluLeuThrGluLeuLeuValValMetLeuLeuThrAlaAr 17

|||||

51 GCTAACGCTGCCAGCCGCTCTCTCGTGGTCATGCTCGAGTCTCTCA 100

|||||

17 gLeuThrLeuSerSerProAlaProProAlaCysAspLeuArgValLeu 34

|||||

101 GTAAACCTGCTTCGTGACTCCCATGCTCTTCACAGCAGACTGAGCGTGC 150

|||||

34 erLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGluCys 50

|||||

151 CCAGAGGTTCACCTCTTGGCTTACACCTGCTGCTGCTGCTGCTGCTGCT 200

|||||

```
51 ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPh 67
201 TAGCTTGGGAGAAATGGAACCCAGATGGAGGAGACCAAGGCACAGACA 250
    |||||
67 eSerLeuGlyLysThrGlnMetGluThrLysAlaGlnAspI 84
251 TTCTGGGAGCAGTACCCTTCTGCTGGAGGAGTGTATGGCAGCAGCGGGA 300
    |||||
84 leLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAaArgGly 100
301 CAACCTGGGACCCACTTGCCTCTCATCCTCTCTGGGCGAGCTTCTGGACA 350
    |||||
101 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGI 117
351 GGTCCGCTCTCTCTGGGCGCTGCGAGAGCTCTCTTGAACCCAGCTTC 400
    |||||
117 nValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuP 134
401 CTCCACAGGGCAGGACACAGCTCACAGGATCCCAATGCCATCTTCCTTG 450
    |||||
134 roProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu 150
451 AGCTTCCACACCTGCTCCGAGGAAAGTCGTTCTCTGATGCTTGTAGG 500
    |||||
151 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGI 167
501 AGGTTCACCTCTGCTAGCGGGGCGCCAAACATATCGCGCTCGAGTC 550
    |||||
167 yGlySerThrLeuCysValArgAlaProThrTyrArgAlaSerSerL 184
551 TACCACAGAGCTTCTTTTAAAAAGCTTAGCAAGTGAGGAAGATCCAG 600
    |||||
184 euProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGln 200
601 GCGCATGGCGCAGGCTCCAGGAGAACTGTGCCACCTACAGCTGTG 650
    |||||
201 GlyAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCy 217
651 CCACCCGAGGAGCTGTGCTCGCACACTCTCTGGGCATCCCTGGG 700
    |||||
217 sHisProGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpA 234
701 CTCCTCTGAGCAGTGCCTCCAGGCGCTCGAGTGGCAGGCTGCTTG 750
    |||||
234 laProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeu 250
751 AGCAACTCCATAGCGCTTCTCTTACCAGGCGCTCTCGAGCGCCT 800
    |||||
251 SerGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLe 267
801 GGAAGGATCTCCCGGAGTTGGTCCACCTTGGACACACTGCAGCTGG 850
    |||||
267 uGluGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuA 284
851 ACGTCGCGGACTTTGCCACCACTATCTGGCAGCAGATGGAAGAACTGGGA 900
    |||||
284 spValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGly 950
901 ATGGCCCTGCGCTGCAGCCCAACCCAGGCTGCCATGCCGCGCTTCGCCCTC 950
    |||||
301 MetAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaLe 317
951 TGCTTTCCAGCGCGGCGAGGAGGGTCTAGTTGCCCTCCCATCTGCAGA 1000
    |||||
317 rAlaPheGlnArgAlaGlyValLeuValAlaSerHisLeuGlnS 334
1001 GCTTCTGGAGGTCTGTACCGGCTTCTACGCCACTTGCACCACTTGCACGCC 1047
    |||||
334 erPheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro 349
    |||||
seq_name: US09680514.pep:US-09-680-514-7
seq_documentation_block:
```

```
; Sequence 7, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotzu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-680-514-7

alignment_scores:
    Quality: 1753.00          Length: 361
    Ratio: 5.023              Gaps: 1
    Percent Similarity: 96.676  Percent Identity: 96.676

alignment_block:
us-09-680-514-4 x US-09-680-514-7 ..
Align seg 1/1 to: US-09-680-514-7 from: 1 to: 361

1 ATGGAGCTGACTGAATGCTCTCTGTTGGTCATGCTCTCTTAAGTCAAG 50
    |||||
1 MetGluLeuThrGluLeuLeuValMetLeuLeuThrAlaAr 17
51 GCTAAGCTGTCCAGCCCGCTCTCTCTGTTGACCTCCGAGTCTCA 100
    |||||
17 gluThrLeuSerSerProAlaProProAlaCysAspLeuArgValLeuS 34
101 GTAAACTGCTTCTGCTACTCCCATGCTCTTTCACAGCAGACTGAGCCAGTGC 150
    |||||
34 erLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys 50
151 CCAGAGGTTACCCCTTGGCTTGCCTACACCTGCTCTGCTGCTGCTGACTT 200
    |||||
51 ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPh 67
201 TAGCTTGGGAGAAATGGAACCCAGATGGAGGAGACCAAGGCACAGACA 250
    |||||
```



```
67  eserLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspI 84
251 TTCTGGGAGCAGTACCTTCTGCTGGAGGAGTGTGGCAGCAGCGGGA 300
84  leLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly 100
301 CAACTGGGACCACTTGCCTCTCATCCTCTCTGGGGAGCTTTCTGGACA 350
101 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyG 117
351 GGTCCGCTCTCTCTGGGGCCCTGCGAGAGCTCTCTTGGAAACCAAGTTC 400
117 nValargLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu 134
401 CTCACAGGGCAGGACACAGCTCACAGAGTCCCAATGCCATCTTCCTG 450
134 roProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu 150
451 AGCTTCCAAACCTGCTCCGAGGAAGTGGTTCCTGTATGCTGTGAGG 500
151 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValG 167
501 AGGTCCACCTCTGCGTACGG ..... 522
167 yGlySerThrLeuCysValArgSerGlyGlySerGlyGlySerG 184
523 .....CGGCGCCAAATATCGCGCTCGAGTCTA 552
184 yGlyGlySerGlyGlyArgAlaProThrTyrArgAlaSerSerLeu 200
553 CCACAGAGTTCCTTTTAAAGCTTAGACAAGTGAAGAGATCCAGGG 602
201 ProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnG 217
603 CGATGGCGCAGCGTCCAGGAGAGCTGTGCCACCTACAGCTGTGCC 652
217 yAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCy 234
653 ACCCGGAGAGCTGGTCTGCTGGACACACTCTCTGGGCATCCCGCTGG 702
234 lsProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAla 250
703 CCCTGAGCAGCTGCCCGCAGCGCCCTGCAGTGGCAGGCTGTGAG 752
251 ProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeu 267
753 CCAACTCCATAGCGGCTTTTCTCTACCGAGGCTCTCTCAGCGCCCTGG 802
267 rGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeu 284
803 AAGGATCTCCCCGAGTTGGTCCCGCTGGACACACTGACAGCTGGAC 852
284 luGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAsp 300
853 GTCGCCGACTTTGCCACCACTCTGCGACAGATGGAAGAACTGGGAAT 902
301 ValAlaaspPheAlaThrIleTrpGlnGlnMetGluLeuGlyMe 317
903 GCGCCCTGCGCTCGACGCCCGCAGGTCGATCCGCGCTTCGCTCTG 952
317 talapAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSerA 334
953 CTTTCCAGCGCGGCGAGAGGGTCTCTAGTTGCTCCCATCTGCGAGAG 1002
334 laPheGlnArgArgAlaGlyValLeuValAlaSerHisLeuGlnSer 350
1003 TTCCTGGAGGTGTGTCACCGGTTCTACGCCACCTTGGCCCGAGCCC 1047
351 PheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro 365
```

seq_name: US09680514.pep:US-09-680-514-1

seq_documentation_block:

```
; Sequence 1, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotzu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-680-514-1

alignment_scores:
    Quality: 1677.00      Length: 328
    Ratio: 5.113          Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
us-09-680-514-4 x US-09-680-514-1 ..

Align seg 1/1 to: US-09-680-514-1 from: 1 to: 328

64  AGCCCGGCTCCTCTGCTGTGACCTCCGAGTCTCAGTAAACTGCTTCG 113
1  SerProAlaProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
114 TGACTCCCATGCTTCACAGCAGACTGAGCCAGTGCCAGAGTTCCACC 163
17  gaspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHis 34
164 CTTTGCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
34  roLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
214 TGGAAACCCAGATGGAGGAGCACAGGACAGGACATCTTGGGAGCAGT 263
51  TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
264 GACCCCTCTGCTGGAGGAGTGTATGTCAGCAGCGGGGACAACTGGGAC 313
```



```
364 CTTGGGGCCCTGCAGAGCTCTTGGAAACCCAGCTTCTCCACAGGGCAG 413
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
414 GACCACAGCTCACAGGATCCCATGCTCCTCAGCTTCCACACC 463
117 gthrThrAlaHisLysaspProAsnAlaIlePheLeuSerPheGlnHisL 134
464 TGCTCCGAGGAAGTGGTTCCTGATGCTGTAGGAGGCTCCACCTC 513
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
514 TGGCTACGG.....CGGC 527
151 CysValArgGlyGlySerGlyGlySerGlyGlyGlySerArgAl 167
528 GCCACATATCGCCCTCGAGTCTTACCACAGAGCTTCTTTAAAAGCT 577
167 aproThrArgAlaSerLeuProGlnSerPheLeuLeuLysSerL 184
578 TAGAGCAAGTGAAGAATCCAGGGCATGGCGAGCGCTCCAGGGAAG 627
184 euGluGlnValArgLysIleGlnGlyaspGlyAlaAlaLeuGlnGluLys 200
628 CTGTGTGCCACCTACAGCTGTGCCACCCCGAGAGAGCTGTGTGCTCGG 677
201 LeuCysAlaThrTrpLysLeuCysHisProGluGluLeuValLeuGlu 717
678 ACACCTCTGGGCATCCCTGGGCTCCCTGAGCAGCTGCCCGCCAGCAGG 727
217 yHisSerLeuGlyIleProThrAlaProLeuSerSerCysProSerGlnA 234
728 CCCTGAGCTGGCAGGTGCTTGAGCAACTCCATAGCGGCTTTTCCTC 777
234 laLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeu 250
778 TACCAGGGCTCTGCAGGCGCTGGAGGATCTCCCGAGTTGGGTCC 827
251 TyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyPr 267
828 CACCTTGACACACTGCAGCTGGAGCTGCGCGACTTTGCCACCACTCT 877
267 othrLeuAspThrLeuGlnLeuaspValAlaAspPheAlaThrThrIle 284
878 GGCAGCAGATGGAAGAACTGGGAATGCCCTGCTGCAGCCACCCAG 927
284 rpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGln 300
928 GGTGCCATGCGGCTTCCGCTCTGCTTCCAGCGCGGGCAGAGGGT 977
301 GlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyVa 317
978 CCTAGTTGCCCTCCATCTGAGAGCTTCTGGAGGTCTGCTACCGGTTTC 1027
317 lleuValaSerHisLeuGlnSerPheLeuGluValSerTyrArgVal 334
1028 TACGCCACCTTGCCCGCC 1047
334 euArgHisLeuAlaGlnPro 340
```

seq_name: US09680514.pep:US-09-680-514-3

seq_documentation_block:

; Sequence 3, Application US/09680514

; GENERAL INFORMATION:

; APPLICANT: Yokoi, Haruhiko

; Shiotsu, Yukimasa

; Konishi, Noboru

; TITLE OF INVENTION: NOVEL POLYPEPTIDES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 North Glebe Rd. 8th floor

```

;
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-680-514-3
```

alignment_scores:

Quality: 1659.00 Length: 344

Ratio: 5.058 Gaps: 1

Percent Similarity: 95.349 Percent Identity: 95.349

alignment_block:

us-09-680-514-4 x US-09-680-514-3 ..

Align seg 1/1 to: US-09-680-514-3 from: 1 to: 344

```
64 AGCCCGGCTCTCTCTGCTGACCTCCGAGTCTCAGTAACTGCTTCG 113
1 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
114 TGACTCCCATGTCTTCACAGCAGACTGAGCCAGTCCCAGAGGTTCCAC 163
17 gapSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
164 CTTTGGCTACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
34 roleuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
214 TCGAAACCCAGATGGAGGACCAAGGCACAGACATTTCTGGGAGCAGT 263
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
264 GACCCCTTCTGCTGGAGGAGTGTATGGCAGCAGCGGACAACTGGGACCA 313
67 lThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProt 84
314 CTTGCTCTCATCCCTCTGGGGCAGCTTCTTGACAGAGTCCGCTCTCCTC 363
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTTGGGGCCCTGCAGAGCTCTCTTGGAAACCCAGCTTCTCCACAGGGCAG 413
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
```

```
414 GACCACAGCTCACAAGATCCCAATGCCATCTCTGAGCTTCCACACC 463
|||||
117 gthrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisL 134
|||||
464 TCCTCCGAGGAAGTGGTTCCTGATGCTGTGTAGGAGGGTCCACCTC 513
|||||
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
|||||
514 TCGCTACGG..... 522
|||||
151 CysValArgSerGlyGlySerGlyGlyGlySerGlyGlySerGly 167
523 .....CGGGCCCAACATATCGCGCTCGAGTCTACACAGAGCTTCC 565
|||||
167 yGlyGlyArgAlaProThrTyArgAlaSerSerLeuProGlnSerPheL 184
|||||
566 TTTTAAAAAGCTTAGACAAGTAGAGATCCAGGGGATGCCAGCG 615
|||||
184 euLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla 200
|||||
616 CTCAGGAGAGCTGTGTGCCACCTACAGCTGTGCCACCCCGAGAGCT 665
|||||
201 LeuGlnGluLysLeuGlyAlaThrTrpLysLeuGlyHisProGluGluLe 217
|||||
666 GGTGCTGCTCGACACTCTCTGGGCATCCCTGGGCTCCCTGAGCAGCT 715
|||||
217 uValLeuLeuGlyHisSerLeuGlyLeuProTrpAlaProLeuSerSerC 234
|||||
716 GCCCAGCAGCCCTGAGCTGGAGCTGCTTGGAGCCAACTCATAGC 765
|||||
234 ysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSer 250
|||||
766 GGCCTTTTCTCTACACGGGCTCTCGAGGCCCTGGAAGGATCTCCCC 815
|||||
251 GlyLeuPheLeuTyGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerPr 267
|||||
816 CGAGTTGGTCCCACCTTTGGACACTCCAGCTGGAGCTGCCCGACTTTG 865
|||||
267 oGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheA 284
|||||
866 CCACACCATCTGGCAGCAGATGGAGACTGGGAATGGCCCTGCCCTG 915
|||||
284 laThrThrIleTrpGlnMetGluGluLeuGlyMetAlaProAlaLeu 300
|||||
916 CAGCCACCCAGGGTGCATCGCGCCTTCGCCTCTGCTTTCCAGCGCGC 965
|||||
301 GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgAr 317
|||||
966 GGCAGGAGGGTCTCTAGTTGGCTCCCATCTGCAGAGCTTCCTGGAGGTGT 1015
|||||
317 gAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValS 334
|||||
1016 CGTACCGGTTCTAGCGCCACTTGCACGCC 1047
|||||
334 ertyrArgValLeuArgHisLeuAlaGlnPro 344
|||||
seq_name: US09680514.pep:US-09-680-514-39
```

```
seq_documentation_block:
; Sequence 39, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: YOKOI, Haruhiko
; Shiotani, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
```

```
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/680,514
FILING DATE: 06-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,337
FILING DATE: <Unknown>
APPLICATION NUMBER: JP P.HEI.7-102625
FILING DATE: 26-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 249-89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-680-514-39

alignment_scores:
Quality: 851.00 Length: 173
Ratio: 5.065 Gaps: 0
Percent Similarity: 97.110 Percent Identity: 97.110

alignment_block:
us-09-680-514-4 x us-09-680-514-39 ..
Align seg 1/1 to: US-09-680-514-39 from: 1 to: 175

529 CCAACATATCGGCTCGAGTCTACCACAGAGCTTCCTTTTAAAAAGGTT 578
|||
3 ProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLe 19
|||||
579 AGAGCAACTGAGGAAGATCCAGGGCGATGGCCAGCGCTCCAGGAGAAGC 628
|||||
19 uGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysL 36
|||||
629 TGTGTGCCACCTACAAAGCTGTGCCACCCCGAGGAGCTGTGTCTCGGA 678
|||||
36 euCysAlaThrTyrlsLeuGlyHisProGluGlyLeuValLeuLeuGly 52
|||||
679 CACTCTGGGCATCCCTGGGCTCCCTGAGCAGCTGCCCGCAGCCAGCC 728
|||||
53 HisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAl 69
|||||
729 CCTGCAGCTGGCAGGCTGCTTGAGCCAACCTCCATAGCGCCTTTTCCTCT 778
|||||
69 aLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuT 86
|||||
779 ACCAGGGCTCTCTGCAGGCCCTTGGGAAGGATCTCCCGGAGTTGGTGTC 828
|||||
86 yrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyPro 102
|||||
829 ACCTTGGACACACTGACGTGAGCTGCCCGACTTTGCCACACCATCTG 878
|||||
103 ThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTr 119
|||||
879 GCAGCAGATGGAGAAGCTGGGAATGGCCCTGCCCTGCAGCCACCCAGG 928
|||||
```

```

119 pGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnG 136
929 GTGCCATCCCGCTTCCCTCTCTCTCCAGCCGCGGAGGAGGGTC 978
136 lYAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyVal 152
979 CTAGTTGGCTCCCATCTGCAGAGCTTCTCGAGGTGTCGTACCGGTCT 1028
153 LeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValLe 169
1029 ACGCCACTTCCCGAGCCC 1047
169 uArgHisLeuAlaGlnPro 175
seq_name: US09680514.pep:US-09-680-514-40

```

```

seq_documentation_block:
; Sequence 40, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
;                Shiotsu, Yukimasa
;                Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION DATE: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-680-514-40

```

```

alignment_scores:
Quality: 835.00 Length: 359
Ratio: 3.422 Gaps: 13
Percent Similarity: 67.967 Percent Identity: 56.825

```

```

alignment_block:
us-09-680-514-4 x US-09-680-514-40
Align seg 1/1 to: US-09-680-514-40 from: 1 to: 332

```

```

64 AGCCCGGCTCCTCCTGTGTGACCTCCGAGTCTCTAAGTAACTGCTTCG 113
1 SerProAlaProAlaCysAspLeuArgValLeuSerLysLeuLeuArg 17
114 TGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGCACAGAGGTTCCAC 163
17 gAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
164 CTTTGGCTACACCTGTCTGTCTGCTGCTGTGGACTTTAGCTTGGAGAA 213
34 roLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
214 TGGAAACCCAGATGGAGGAGACCAAGGCACAGACATTTCTGGAGCAGT 263
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
264 GACCCCTCTCTCGAGGGAGTGATGGCAGCAGCGGGACAACTGGGACCCA 313
67 lThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProt 84
314 CTTGCTCTCTATCCCTCCTGGGCAGCTTTCTGGACAGGTCCCTCTCCTC 363
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTTGGGGCCCTGCAGAGCCTCTCTTGGAAACCCAGCTTCTCCACAGGCAG 413
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArg 117
414 GACCACAGCTCAAGATGCCAATGCCATCTTCTGAGCTTCCAGCTTCCAAC 463
117 gThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisL 134
464 TGCTCCGAGGAAAGGTGCGTTTCTCTGATGCTTGTAGGAGGTCCACCCCTC 513
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
514 TGGGTACGGCGGGCCCAACATATCGCGCTCGAGTCTACACAGAGCTT 563
151 CysValArgArgAlaProProThrThrAlaValProSerArgThrSerLe 167
564 CCTTTTAAAGCTTAGACCAAGTGAGGAGATCCAGGGCGGATGGCCGAG 613
167 uValLeuThrLeuAsnGluLeuProAsnArgThrSerGly.....L 181
614 CGTCCAGGAGAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAG 663
181 euLeuGluThrAsnPheThrAlaSerAlaArg..... 191
664 CTGGTCTCTCGGACACTCTCTGGGCATCCCTCGGCTCCC..... 705
192 .....ThrThrGlySerGlyLeu...LeuLysTrpGlnGlnGlyPheAr 205
706 .....CTGAGCAGCTGCCCCAGCCAGGCCCTG...CAGC 736
205 gAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnI 222
737 TGGCAGGCTCTTGAGCAACTCCATCATAGCGGCTTTTCTCTACACAGG... 784
222 leProGlyTyrLeuAsnArgIleHisGluLeuLeu.AsnglyThrArgGl 238
785 .....GGCTCTCGAGGCCCTCGGAGGAGGATCTCC..... 814
238 yLeuPheProGlyProSerArgThrLeuGlyAlaProAspIleSerS 255
815 .....CCGAGTTGG 823
255 erGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyr 271
824 GTCCCACTTGGACACACTGCAGCTGGAGTCCCGACTTTGCCACACCC 873
272 SerProSerProThrHis.....ProPr 279
874 ATCTGGCAGCAGATGGAAGAACTGGGAATGGCCCTGCCCCTGCAGCCAC 923

```



```

213 Glyasp.....GlyAlaAlaLeuGlnGlu 221
397 GCTGGTTCACAGGAGGCTCTGACGGCCCCCAAGGAGGAGACGACCTGT 348
||||::: ||| |||::: |||::: |||::: |||::: |||:::
221 sLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuG 238
347 CCAGAAAGCTGCCCCAGGAGGATGACGACCAAGTGGGTCCCAAGTTGTCC 248
::: ::: |||
238 lyHisSerLeu.....GlyIleProThrAlaProLeuSer 249
297 CCGTGTGCCATCACTCCCTCCAGCAAGGGTCACTGCTCCCAAGAATGT 260
||||::: ||| |||::: ||| |||
250 SerCysProSerGlnAlaLeuGlnLeuAlaGly..... 260
247 CCTGTGCTTGGTCTCTCCATCTGGGT 220
||||::: ||| ||| |||
261 ...CysLeuSerGlnLeuHisSerGly 268

seq_name: US09680514.pap:US-09-680-514-9

seq_documentation_block:
; Sequence 9, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotzu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; City: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-680-514-9

alignment_scores:
Quality: 87.50 Length: 264
Ratio: 0.803 Gaps: 15
Percent Similarity: 41.288 Percent Identity: 26.894

alignment_block:
us-09-680-514-4/rev x US-09-680-514-9

```



```
654 GTGGCACAGCTTGTTAGTGGCGCACAGCTT..... 625
::: ||| ::| ||||| |||||
103 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 119
624 ....CTCTGGAGCGCTGGCCATCGCCCTGGATCTTCCTCACTGCTCT 579
::: ||| ::| ||||| |||||
119 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 135
578 AAGCTTTTAAAGGAAGCTGTGTGTAGACTCGAGGC..... 541
136 .....ArgGlyLysValArgPhe 141
540 .....GCGATAGTTGGCGCCGCCGTACGCAGA 512
142 LeuMetLeuValGlySerThrLeuCysValArg..... 153
511 GGGTGGACCTCTACAAGCATCAG.....GAAAGCGACCTT..... 475
154 .ArgAlaProThrTyrArgAlaSerSerLeuProGlnSerPheLeuLeuL 170
474 ..TCCTCGGAGCAGGTGTGAAGCTCAGGAAGATGGCATGGATCCTT 427
170 ysSerLeuGlnValArgLysIleGlnGlyAsp..... 181
426 GTGAGCTGTGTCTGCTGCTGGAGGAGCTGCTTCCAGAGGCTCT 377
182 .....GlyAlaAlaLeuGlnLysLeuCysAlaThrTyrLysLe 195
376 GCAGGGCCCCAAGGAGGAGGAGGACCTCCAGAAAGCTGCCAGGAGG 327
195 ucYshisProGluGlnLeuLeuLeuGlyHisSerLeu..... 208
326 GATGAGAGGCAAGTGGTCCCGTGTCTCCCGTGTGCATCATCCCTC 277
209 .....GlyLeuProThrAlaProLeuSerCysProSerGlnAlaLeu 223
276 CAGCAGAAAGGTCTACTGTCTCCAGAAATCTCTGCTGCTGCTGCTCC 227
224 GlnLeuAlaGly.....CysLeuSerGlnLeuHi 233
226 TCTGGGT 220
233 sSerGly 235

seq_name: US09680514.pep:US-09-680-514-5

seq_documentation_block:
; Sequence 5, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
```

```
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-680-514-5

alignment_scores:
Quality: 82.50 Length: 253
Ratio: 0.778 Gaps: 15
Percent Similarity: 41.897 Percent Identity: 27.273

alignment_block:
us-09-680-514-4/rev x US-09-680-514-5 ..
Align seg 1/1 to: US-09-680-514-5 from: 1 to: 349

838 TGTCCAGTGGGACCCAACTCGGGGAGATCCCTTCCAGGCGCTGCAGG 789
|||||::: ||| ||||| |||||
50 CysProGluValHisPro.....LeuProThrProValLe 61
788 AGCCCT.....GCTAGAGAAAGCGCGCTATGCAG 757
||| ||| ||| ||| ||| ||| ||| |||
.61 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 77
756 TTGGCTCAAGCAGCTGCAGCTGCAGGCGCTGCTGGGCA..... 715
::: ||| ||| ::| |||||
78 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 90
714 .....GCTGCTCAGGGAGCGCCAGGGAT..... 691
|||||::: ||| |||
90 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 107
690 .....GCCAGAGAGTGTCCGAGCAGCAGCAGCTCCTCGG 655
107 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 123
654 GTGGCACAGCTTGTTAGTGGCACACAGCTT..... 625
::: ||| ::| ||||| |||||
124 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 140
624 ....CTCTGGAGCGCTGGCCATCGCCCTGGATCTTCCTCACTGCTCT 579
::: ||| ::| ||||| |||||
140 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 156
578 AAGCTTTTAAAGGAAGCTGTGTGTAGACTCGAGGC..... 541
157 .....ArgGlyLysValArgPhe 162
540 .....GCGATAGTTGGCGCCGCCGTACGCAGA 512
163 LeuMetLeuValGlySerThrLeuCysValArg..... 174
511 GGGTGGACCTCTACAAGCATCAG.....GAAAGCGACCTT..... 475
175 .ArgAlaProThrTyrArgAlaSerSerLeuProGlnSerPheLeuLeuL 191
474 ..TCCTCGGAGCAGGTGTGAAGCTCAGGAAGATGGCATGGATCCTT 427
191 ysSerLeuGlnValArgLysIleGlnGlyAsp..... 202
```



```

315 AGTGGGTCCAGTTGTCCCGTGTGCTGCATCCTCCCTCCAGCAGAGGG 266
:: :::: ::::: ::::: |||
245 rArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGly 261
265 TCACTGTCTCCAGAA.....TGTCCTGTGCCTTGCTCTCC 231
||||| ||::: ||| |||
262 SerLeuProProAsnLeuGlnProGlyTyrSerProSerProThrHisPr 278
230 TCCATCTGGG...TTTCCATTCTCCCA 206
||||: ||| ::::: |||
278 oProThrGlyGlnTyrThrLeuPhePro 287

```


OM of: us-09-680-514-6 to: US09680514.pep:* out_format : pfs
Date: Apr 8, 2002 2:23 PM
About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=framet_n2p.model -DEV=xlp -O=us-09-680-514-6
-DB=US09680514.pep -OUT=align_6_pep.res -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-XGAPOP=4.500 -XGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-XGAPOP=6.000 -XGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUT=pf
-NORM=ext -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -ICPU=3 -LONGLOG
-NO_XLPXY -THREADS=1

Search information block:
Query: us-09-680-514-6
Query length: 1083
Database: US09680514.pep:*
Database sequences: 24
Database length: 2736
Search time (sec): 3.220000

score_list:	Sequence	Strd Orig	Zscore	EScore	Len	Documentation
	US09680514.pep:US-09-680-514-7	1835.00	1291.17	3.1e-69	361	Sequence 7, Applicat
	US09680514.pep:US-09-680-514-8	1813.00	1275.48	2.3e-68	365	Sequence 9, Applicat
	US09680514.pep:US-09-680-514-9	1753.00	1233.29	5.4e-66	349	Sequence 5, Applicat
	US09680514.pep:US-09-680-514-2	1743.00	1226.41	1.3e-65	340	Sequence 2, Applicat
	US09680514.pep:US-09-680-514-3	1721.00	1210.71	9.9e-65	344	Sequence 3, Applicat
	US09680514.pep:US-09-680-514-1	1661.00	1168.54	2.3e-62	328	Sequence 1, Applicat
	US09680514.pep:US-09-680-514-39	851.00	599.11	2.3e-30	175	Sequence 30, Applic
	US09680514.pep:US-09-680-514-40	819.00	571.23	4.2e-29	332	Sequence 40, Applic
	US09680514.pep:US-09-680-514-3	90.50	54.24	2.19	344	Sequence 9, Applicat
	US09680514.pep:US-09-680-514-9	90.50	53.76	2.17	365	Sequence 3, Applicat
	US09680514.pep:US-09-680-514-2	86.50	51.50	2.96	340	Sequence 2, Applicat
	US09680514.pep:US-09-680-514-7	86.50	51.01	2.92	361	Sequence 7, Applicat
	US09680514.pep:US-09-680-514-1	83.50	48.95	3.92	328	Sequence 1, Applicat
	US09680514.pep:US-09-680-514-5	82.50	48.45	3.85	349	Sequence 5, Applicat
	US09680514.pep:US-09-680-514-24	71.00	66.89	12.99	13	Sequence 24, Applicat
	US09680514.pep:US-09-680-514-42	66.00	63.99	20.11	12	Sequence 44, Applicat
	US09680514.pep:US-09-680-514-21	66.00	61.67	20.01	16	Sequence 42, Applicat
	US09680514.pep:US-09-680-514-35	66.00	61.18	19.97	17	Sequence 35, Applicat
	US09680514.pep:US-09-680-514-40	62.00	34.31	8.04	332	Sequence 40, Applic
	US09680514.pep:US-09-680-514-15	48.00	0.00	338.75	8	Sequence 15, Applicat
	US09680514.pep:US-09-680-514-17	48.00	0.00	338.75	8	Sequence 17, Applicat
	US09680514.pep:US-09-680-514-39	48.00	0.00	338.75	8	Sequence 39, Applicat
	US09680514.pep:US-09-680-514-26	45.00	0.00	301.11	9	Sequence 26, Applicat
	US09680514.pep:US-09-680-514-31	44.00	0.00	338.75	8	Sequence 31, Applicat
	US09680514.pep:US-09-680-514-38	44.00	0.00	338.75	8	Sequence 45, Applicat
	US09680514.pep:US-09-680-514-23	42.00	0.00	338.75	8	Sequence 33, Applicat
	US09680514.pep:US-09-680-514-42	34.00	38.97	152.56	16	Sequence 28, Applicat
	US09680514.pep:US-09-680-514-35	34.00	38.48	145.79	17	Sequence 35, Applicat
	US09680514.pep:US-09-680-514-44	32.00	39.88	186.94	12	Sequence 44, Applicat
	US09680514.pep:US-09-680-514-21	32.00	39.23	186.14	13	Sequence 24, Applicat
	US09680514.pep:US-09-680-514-24	23.00	0.00	338.75	8	Sequence 21, Applicat
	US09680514.pep:US-09-680-514-31	23.00	0.00	338.75	8	Sequence 31, Applicat
	US09680514.pep:US-09-680-514-33	23.00	0.00	338.75	8	Sequence 33, Applicat
	US09680514.pep:US-09-680-514-15	22.00	0.00	338.75	8	Sequence 15, Applicat
	US09680514.pep:US-09-680-514-17	22.00	0.00	338.75	8	Sequence 17, Applicat
	US09680514.pep:US-09-680-514-45	22.00	0.00	338.75	8	Sequence 45, Applicat
	US09680514.pep:US-09-680-514-26	22.00	0.00	301.11	9	Sequence 26, Applicat
	US09680514.pep:US-09-680-514-19	20.00	0.00	338.75	8	Sequence 19, Applicat
	US09680514.pep:US-09-680-514-21	20.00	0.00	338.75	8	Sequence 21, Applicat
	US09680514.pep:US-09-680-514-19	18.00	0.00	338.75	8	Sequence 19, Applicat
	US09680514.pep:US-09-680-514-28	17.00	0.00	338.75	8	Sequence 28, Applicat

seq_name: US09680514.pep:US-09-680-514-7
seq_documentation_block:
; Sequence 7, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Noboru
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P. HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-680-514-7

alignment_scores:
Quality: 1835.00 Length: 361
Ratio: 5.083 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
us-09-680-514-6 x US-09-680-514-7
Align seg 1/1 to: US-09-680-514-7 from: 1 to: 361

1 ATGAGCTGACGTGAATTCTCTCTGTCATGCTTCTCCTAAGTCAAG 50
|||||
1 MetGluLeuThrGluLeuLeuValMetLeuLeuLeuThrAlaAr 17
|||||
51 GCTAACGCTGCCAGCCGGCTCTCTCTGCTGTGACCTCCGAGTCCTCA 100
|||||
17 gLeuThrLeuSerGluProAlaProAlaCysAspLeuArgValLeu 34
|||||
101 GTAAAGTCTTTCGTGACCTCCCATGCTCTTACAGCAGACTGAGCAGTGC 150
|||||
34 erLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys 50
|||||
151 CCAGAGGTTACCCCTTTGCCTACACCTGCTCTGCTGCTGCTGAGACTT 200
|||||

51 ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPh 67
201 TAGCTTGGAGAAATGGAACCCAGATGGAGGACCAAGCCAGCAGACA 250
67 eSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspI 84
251 TTCGGGAGCAGTAGTACCCTTCTGCTGGAGGAGTAGTGAGCAGCAGCGGA 300
84 leLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly 100
301 CAACCTGGGACCACTTGCCTCTCATCCTCTCTGGGCGAGCTTCTGGACA 350
101 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGI 117
351 GGTCCGTCTCTCTCTGGGGCCCTGCGAGAGCTCTCTTGGAAACCCAGCTTC 400
117 nValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuP 134
401 CTCCACAGGCGAGCACACAGCTCACAAAGGATCCCAATGCCATCTTCCTG 450
134 roProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu 150
451 AGCTTCCAAACACCTGCTCCGAGGAAAGTGGTTCCTGATGCTGTAGG 500
151 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGI 167
501 AGGTGCCACCTCTCGCTGCGTCAGGGGTGGCTTCTGGAGGTGGTTCGGAG 550
167 yGlySerThrLeuGlyValArgGlyGlySerGlyGlySerGlyGly 184
551 GGGGTTCCTAGAGCACCAACATATCGCGCTCGAGTCTGATGCTACACAGCTTC 600
184 yGlySerArgAlaProThrTyrArgAlaSerSerLeuProGlnSerPhe 200
601 CTTTAAACCTTAGCAGCAGTACGAGGATCCAGGCGGATCGCCAGC 650
201 LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAI 217
651 GCTCCAGGAGAGCTGTGTGCCACTACAAGCTGTGCGACCCCGAGAGC 700
217 aLeuGlnLysLeuGlyAlaThrTyrLysLeuGlyHisProGluGluL 234
701 TGGTGTCTCGGACACTCTCTGGGCAATCCCTGGGCTCCCTCGAGCAGC 750
234 euValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSer 250
751 TGCCCCAGCCAGCCCTGCGAGCTGGAGGCTGTGAGCCCACTCCATAG 800
251 CysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSe 267
801 CGGCTTTTCTCTACAGGGGCTCTGCGAGGCTGGAGGATCTCCC 850
267 rGlyLeuPheLeuThrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerP 284
851 CCGAGTTGGGTCCACCTTGGACACACTGAGCTGGAGCTGGCCGACTTT 900
284 roGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe 300
901 GCCACCACTCTGGCAGCAGATGGAAGAACTGGGAATGGCCCTCGCCT 950
301 AlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMetAlaProAlaLe 317
951 GCAGCCCAAGGAGGTGCCATGCGGCTTTCGCTCTGCTTTCCAGCGCC 1000
317 uGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgA 334
1001 GGGCAGGAGGGGTCTAGTGTCCCTCCCATCTGCAGAGCTTCCTGGAGGTG 1050
334 rGAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluVal 350
1051 TCGTACCGCGTTCTACGCCACCTTGCCGCCAGCCC 1083
351 SerTyrArgValLeuArgHisLeuAlaGlnPro 361

seq_name: US09680514.pep:US-09-680-514-9
seq_documentation_block:
; Sequence 9, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotzu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-680-514-9

alignment_scores:
Quality: 1813.00 Length: 365
Ratio: 5.022 Gaps: 2
Percent Similarity: 98.904 Percent Identity: 98.904

alignment_block:
us-09-680-514-6 x us-09-680-514-9 ..
Align, seg 1/1 to: US-09-680-514-9 from: 1 to: 365
1 ATGGAGCTGACTGAATTGCTCTGCTGGTCAATGCTTCTCCTAACTGCAAG 50
|||||
1 MetGluLeuThrGluLeuLeuValValMetLeuLeuLeuThrAlaAr 17
51 GCTAACGCTGCTCCAGCCCGGCTCTCTGCTGTGAGCTCCGAGTCCCTCA 100
|||||
17 gLeuThrLeuSerSerProAlaProAlaCysAspLeuArgValLeuS 34
101 GTAACTGCTTGTGACTCCCATGCTCTTCCACAGCAGACTGAGCCAGTGC 150
|||||
34 erLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys 50
151 CCAGAGGTTTCACCTTTGCTGTACACCTGCTGCTGCTGCTGCTGCTG 200
|||||

seq_name: US09680514.pep:US-09-680-514-5

```
51 ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPh 67
201 TAGCTTGGAGAAATGGAACCCAGATGGAGGAGACCAAGCAGCAGACA 250
|||||
67 eserLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspI 84
|||||
251 TTCTGGGAGCAGTACCCTTCTGCTGGAGGAGTGTGGCAGCAGCGGGA 300
|||||
84 leLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly 100
|||||
301 CAACTGGGACCACTTGCTCTCATCTCTCTGGGAGCTTCTTGAGACA 350
|||||
101 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyG 117
|||||
351 GGTCTGCTCTCTCTGGGGCCCTGCAGAGCTCTCTTGGAAACCCAGCTC 400
|||||
117 nValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuP 134
|||||
401 TTCCACAGGGCAGGACCACTCACAGGTCCAAAGATCCCAATGCATCTTC 450
|||||
134 roProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu 150
|||||
451 AGCTTCCAAACACCTGCTCCGAGGAAAGTGGTTCTCTGATGCTGTAGG 500
|||||
151 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValG 167
|||||
501 AGGTTCCACCTCTCGCTCAGGGTGGCGGTCTGTGGAGGTGGTTCCGGAG 550
|||||
167 yGlySerThrLeuCysValArg..... 174
|||||
551 GGGGTTCTAGAGCAACCAATATCGCCCTCGAGTCTACCAAGAGGTTTC 600
|||||
175 .....ArgAlaProThrTyrArgAlaSerSerLeuProGlnSerPhe 188
|||||
601 CTTTTAAAGCTTAGAGCAAGTCAGGAAGATCCAGGCGGATGCGCGAGC 650
|||||
189 LeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaI 205
|||||
651 GCTCCAGGAGAGCTGTGTGCCACTCAAGCTGTGTGCCACCCGAGGAGC 700
|||||
205 aLeuGlnLulysLeuCysAlaThrTyrLysLeuCysHisProGluGluL 222
|||||
701 TGGTGTCTCGGACACTCTCTGGGATCCCTGGGCTCCCTCGAGGAGC 750
|||||
222 euValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSer 238
|||||
751 TGCCCCAGCCAGCCCTGCAGCTGGCAGGTGCTTGAGCCAACCTCCATAG 800
|||||
239 CysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSe 255
|||||
801 CGGCTTTTCTCTACCAAGGGCTCTGCAGGCGCTGGAGGCTGATCTCC 850
|||||
255 rGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerP 272
|||||
851 CCGAGTTGGTCCACCTGGACACTGCAGCTGGAGCTCGCGACTTT 900
|||||
272 roGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe 288
|||||
901 GCCACCACTCTGGCAGCAGATGGAAGAACTGGGAATGGCCCTCGCCCT 950
|||||
289 AlaThrThrIleTrpGlnMetGluLeuGlyMetAlaProAlaLe 305
|||||
951 GCAGCCCAACCCAGGGTGCATGGCGGCTTTCGCTCTGCTTCCAGCGCC 1000
|||||
305 uGlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgA 322
|||||
1001 GGGCAGGAGGGTCTAGTTGCTCTCCATCTGCAGAGCTTCTTGGAGGTG 1050
|||||
322 rgAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluVal 338
|||||
1051 TCGTACCGCGTTCTACGCCACCTTGGCCAGGCC 1083
|||||
339 SerTyrArgValLeuArgHisLeuAlaGlnPro 349
```

seq_name: US09680514.pap:US-09-680-514-2

seq_documentation_block:

Sequence 2, Application US/09680514

GENERAL INFORMATION:

APPLICANT: Yokoi, Haruhiko

Shiotzu, Yukimasa

Konishi, Noboru

TITLE OF INVENTION: NOVEL POLYPEPTIDES

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 North Glebe Rd. 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/680,514

FILING DATE: 06-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/765,337

FILING DATE: <Unknown>

APPLICATION NUMBER: JP P.HEI.7-102625

FILING DATE: 26-APR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R.

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 249-89

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-680-514-2

alignment_scores:

Quality: 1743.00

Ratio: 5.126

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

us-09-680-514-6 x US-09-680-514-2

Align seg 1/1 to: US-09-680-514-2 from: 1 to: 340

```
64 AGCCCCGGCTCTCTCTGCTGTGACCTCCGAGTCTCAGTAACTGCTTCG 113
|||||
1 SerProAlaProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
|||||
114 TGACTCCCTGTCTTCACAGCAGCTGAGCCAGTGCACAGAGTTTCACC 163
|||||
17 gasPserHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
|||||
164 CTTTGTGCTACACCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
|||||
34 roleuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
|||||
214 TGGAAACCCAGATGGAGGAGCAGGACAGGACATCTTCTGGAGCAGT 263
```

```
|||||
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
264 GACCTCTCTGCTGGAGGAGTGATGGACGACGGGACAACTGGGACCCA 313
|||||
67 lThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProT 84
314 CTTCGCCCTCATCCCTCCTCGGGAGCTTTCTGGACAGTCCGCTCCTC 363
|||||
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTTCGGGCCCTGCAGAGCCTCTTGGAAACCAGCTTCTCCACAGGGCAG 413
|||||
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
414 GACCACAGCTCACAAAGATCCCAATGCCATCTTCTGAGCTTCCAACACC 463
|||||
117 gThrThraHisLysAspProAsnAlaIlePheLeuSerPheGlnHisL 134
464 TGCTCCGAGGAAAGTGGCTTCTGTATGCTGTAGGAGGTCCACCCCTC 513
|||||
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
514 TGCCTCAGGGTGGCGGTCTTGGAGGTGGTTCCGGAGGGGTTCTAGACC 563
|||||
151 CysValArgGlyGlySerGlyGlyGlySerGlyGlySerArgAl 167
564 ACCAACATATCGCGCTCGAGCTCTACACAGAGCTTCTTTTAAAGCT 613
|||||
167 aProThrTyrArgAlaSerSerLeuProGlnSerPheLeuLeuLysSerL 184
614 TAGACGAAGTGAGGAAGATCCAGGCGGATGGCGAGCGCTCCAGGAGAAG 663
|||||
184 euGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLys 200
664 CTGTGTGCCACTACAGCTGTGCCACCCCGAGGAGCTGTGTGCTCGG 713
|||||
201 LeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuL 217
714 ACATCTCTGGGCATCCCTGGGCTCCCTCGAGCAGCTGCCCGCCAGG 763
|||||
217 yHisSerLeuGlyIleProThrAlaProLeuSerSerCysProSerGlnA 234
764 CCCTGCAGCTGGCAGCTGTGTGACCACTCCATAGCGGCTTTTCTC 813
|||||
234 laLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeu 250
814 TACCAGGGCTCTGCAGGCGCTGGAGGATCTCCCGGAGTGGGTCC 863
|||||
251 TyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyPr 267
864 CACCTTGGACACACTGCAGCTGGAGCTGGCGACTTTGCCACCACTCT 913
|||||
267 oThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIle 284
914 GGCACAGATGGAAACTGGGAATGGCCCTGCCCTGCAGCCCAACCCAG 963
|||||
284 rpGlnMetGluGluGlyMetAlaProAlaLeuGlnProThrGln 300
964 GGTCCATGGCGGCTTCGCTCTGCTTTCCAGCGCGGGCAGAGGGGT 1013
|||||
301 GlyAlaMetProAlaPheAlaSerAlaPheGlnArgAlaGlyGlyVa 317
1014 CCTAGTTGCCCTCCATCTGCAGAGCTTCTGGAGGTGTCTGACCGGCTC 1063
|||||
317 lLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValL 334
1064 TACGCCACCTTGCACGCC 1083
|||||
334 euArgHisLeuAlaGlnPro 340
```

seq_name: US09680514.pep:US-09-680-514-3

```
seq_documentation_block:
; Sequence 3, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-680-514-3

alignment_scores:
Quality: 1721.00 Length: 344
Ratio: 5.062 Gaps: 2
Percent Similarity: 98.837 Percent Identity: 98.837

alignment_block:
us-09-680-514-6 x US-09-680-514-3
..
Align seg 1/1 to: US-09-680-514-3 from: 1 to: 344
64 AGCCCGGCTCCTCCTGCTGTGACCTCCGAGTCTCAGTAACTGCTTCG 113
|||||
1 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
114 TGACTCCCATGCTCCTTCACAGCAGACTGAGCCAGTGCAGAGGTTCA 163
|||||
17 gAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
164 CTTTGCCTACACCTGCTCCTGCTGCTGCTGTGGACTTTAGCTTGGG 213
|||||
34 roLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
214 TGGAAACCCAGATGGAGGAGACCAAGCAGGACATCTCTGGGAGCAG 263
|||||
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
```

```
264 GACCTCTCTGCTGAGGAGTGTGGCAGACCGGGACAACTGGGACCCA 313
    |||
67 lThrLeuLeuLeuGluGlyValMetAlaAaArgGlyGlnLeuGlyPro 84
    |||
314 CTTCCTCTCATCTCCTCTGGGAGCTTTCTGGACAGTTCCTCTCTC 363
    |||
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeu 100
    |||
364 CTTCGGGCTTCGACAGCCCTCTTGGAAACCCAGCTTCCTCCACAGG 413
    |||
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
    |||
414 GACCACAGCTCACAGGATCCCAATGCCATCTCTCTGAGCTTCCACACC 463
    |||
117 gThrThraHisLysAspProAsnAlaIlePheLeuSerPheGlnHis 134
    |||
464 TGCTCCGAGGAAGTGGCTTCCTGATGCTGTAGGAGGTCCACCCCTC 513
    |||
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThr 150
    |||
514 TGCCTCAGG...GGTGGCGGTTCCTGGAGGTGGTTCGGAGGGGTTC 558
    |||
151 CysValArgSerGlyGlySerGlyGlySerGlyGlySerGlyGlySer 167
    |||
559 .....AGACCACCATATCCGCTCGAGTCTACACAGAGCTTCC 601
    |||
167 yGlyGlyArgAlaProThrTyrArgAlaSerSerLeuProGlnSerPhe 184
    |||
602 TTTTAAAGCTTACAGCAAGTGGAGGATCCAGGCGGATGCGCAGCG 651
    |||
184 euLeuLysSerLeuGlnValArgLysIleGlnGlyAspGlyAlaAla 200
    |||
652 CTCAGGAGAGCTGTGTGCACCTACAAGCTGTGCCACCCCGAGGAGCT 701
    |||
201 LeuGlnGlnLysLeuCysAlaThrTyrLysLeuCysHisProGluGlu 217
    |||
702 GGTCTCTGGACACACTCTCTGGGCATCCCTGGCTCCCTCAGCAGCT 751
    |||
217 uValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSer 234
    |||
752 GCCCAGCAGGCTCCTCAGCTGGCAGCTGTGTAGCCAACTCCATAGC 801
    |||
234 ysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSer 250
    |||
802 GGCCTTTTCTCTACAGGGCTCTCTGAGGCTTGGAGGGATCTCCCC 851
    |||
251 GlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSer 267
    |||
852 CGAGTTGGTCCCACTTGGACACTGACGTGGAGCTGCGCGGACTTGG 901
    |||
267 oGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPhe 284
    |||
902 CCACCACATCTGCACACATGAGAACTGGGAATGCCCTCGCCCTG 951
    |||
284 laThrThrIleTrpGlnGlnMetGluLeuLeuGlyMetAlaProAlaLeu 300
    |||
952 CAGCCACCCAGGCTGCATCGCGGCTTCGCTCTGCTTTCAGCGCCG 1001
    |||
301 GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArg 317
    |||
1002 GGCAGGAGGGTCTAGTTCCTCCCATCTGACAGCTTCTCTGGAGGTG 1051
    |||
317 gAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluVal 334
    |||
1052 CGTACCGCTTCTACGCCACCTTGCCAGGCC 1083
    |||
334 erTyrArgValLeuArgHisLeuAlaGlnPro 344
    |||
```

seq_name: US09680514.pep:US-09-680-514-1

seq_documentation_block:

; Sequence 1, Application US/09680514

; GENERAL INFORMATION:

```
314 CTTGGCTCTCATCCTCCTCGGGAGCTTTCTGGACAGGTCGGTCTCCTC 363
|||||
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
|||||
364 CTTGGGGCCCTGCAGAGCCTCTTGGAAACCAGCTTCTCCACAGGGCAG 413
|||||
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
|||||
414 GACCACAGCTCACAGGATCCCATGCTCTCTGAGCTTCCAACACC 463
|||||
117 gThrThrAlaHisLysaspProAsnAlaIlePheLeuSerPheGlnHisL 134
|||||
464 TGCTCCGAGGAAAGTGTGTTCTGATGCTGTGTAGGAGGCTCCACCTC 513
|||||
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
|||||
514 TGCTCAGGGGTGGGGTCTTGGAGGTGGTTCGCGAGGGGGTTCTAGAGC 563
|||||
151 CysValArg.....ArgAl 155
564 ACCAATATCGCCCTCGAGCTTACCACAGAGCTTCTTTTAAAGCT 613
|||||
155 aProThrTyrArgAlaSerSerLeuProGlnSerPheLeuLeuLysSerL 172
|||||
614 TAGACAAGTGAGGAAGATCCAGGGCGATGGCGAGGCTCCAGGAGAAG 663
|||||
172 euGluGlnValArgLysIleGlnGlyaspGlyAlaAlaLeuGlnGluLys 188
|||||
664 CTGTGTGCCACTACAGCTGTGCCACCCGAGAGCTGGTGTCTCGG 713
|||||
189 LeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuLeuL 205
|||||
714 ACCTCTCTGGGCATCCCTGGGCTCCCTGAGCAGCTGCCCGCCAGCAGG 763
|||||
205 yHisSerLeuGlyIleProThrAlaProLeuSerSerCysProSerGlnA 222
|||||
764 CCTGTGAGCTGGCAGGCTGTGTGAGCAACTCCATAGCGGCTTTTCTC 813
|||||
222 laLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeu 238
|||||
814 TACCAGGGCTCTGCGAGGCCCTGGAGGATCTCCCGAGTTGGGTCC 863
|||||
239 TyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyPr 255
|||||
864 CACCTTGGACACACTGCAGCTGGAGCTGGCGACTTTGCCACCAACCATCT 913
|||||
255 oThrLeuaspThrLeuGlnLeuaspValAlaaspPheAlaThrThrIleT 272
|||||
914 GGCAGCAGATGGAAGAACTGGGAATGGCCCTGCGCTGCAGCCCAACCCAG 963
|||||
272 rpGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGln 288
|||||
964 GGTGCCATGCGGGCTTCGCTCTGCTTTCAGCGCCGGGAGGAGGGT 1013
|||||
289 GlyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyVa 305
|||||
1014 CCTAGTTGGCTCCCATCTGCAGAGCTTCTCGAGCTGTCTGTAACCGCTTC 1063
|||||
305 lLeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyrArgValL 322
|||||
1064 TAGCCCACTTGGCCAGCC 1083
|||||
322 euArgHisLeuAlaGlnPro 328
|||||
```

seq_name: US09680514.pep:US-09-680-514-39

seq_documentation_block:

; Sequence 39, Application US/09680514

; GENERAL INFORMATION:

; APPLICANT: Yokoi, Haruhiko

; Shiotzu, Yukimasa

; Konishi, Noboru

```

;
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 45
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: NIXON & VANDERHVE P.C.
;
; STREET: 1100 North Glebe Rd. 8th floor
;
; CITY: Arlington
;
; STATE: VA
;
; COUNTRY: USA
;
; ZIP: 22201-4741
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/09/680,514
;
; FILING DATE: 06-Oct-2000
;
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: 08/765,337
;
; FILING DATE: <Unknown>
;
; APPLICATION NUMBER: JP P.HEI.7-102625
;
; FILING DATE: 26-APR-1995
;
; ATTORNEY/AGENT INFORMATION:
;
; NAME: Crawford, Arthur R.
;
; REGISTRATION NUMBER: 25,327
;
; REFERENCE/DOCKET NUMBER: 249-89
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: 703-816-4000
;
; INFORMATION FOR SEQ ID NO: 39:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 175 amino acids
;
; TYPE: amino acid
;
; STRANDEDNESS: <Unknown>
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: peptide
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
;
; US-09-680-514-39
;

```

alignment_scores:

Quality: 851.00 Length: 173
Ratio: 5.065 Gaps: 0
Percent Similarity: 97.110 Percent Identity: 97.110

alignment_block:

us-09-680-514-6 x us-09-680-514-39 ..

Align seg 1/1 to: US-09-680-514-39 from: 1 to: 175

```
565 CCAACATATCGCGCTCGAGTCTACCACAGAGCTTCTTTTAAAAAGCTT 614
||| |||||
3 ProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLe 19
|||||
615 AGACCAAGTGAAGATCCAGGCGATGGCGCAGCGCTCCAGGAGAAC 664
|||||
19 uGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysL 36
|||||
665 TGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTCTCTCGGA 714
|||||
36 euCysAlaThrTyrLysLeuCysHisProGluGlyLeuValLeuLeuGly 52
|||||
715 CACTCTCTGGGCATCCCTCGGCTCCCTGAGCAGCTGCCCGCCAGCCAGGC 764
|||||
53 HisSerLeuGlyIleProThrAlaProLeuSerSerCysProSerGlnAl 69
|||||
765 CCGCAGCTGGCAGCTGTGAGCAACTCCATAGCGGCTTTTCTCTCT 814
|||||
69 aLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeuT 86
|||||
815 ACCAGGGCTCTCGAGGCTTGAAGGATCTCCCGGAGTTGGGTCCC 864
|||||
```

```

86 yrGlnGlyLeuLeuGlnAlaLeuGluGlyLeuSerProGluLeuGlyPro 102
865 ACCTTGGACACACTGCAGCTGGAGTGGCGGACTTTGGCCACCATCTG 914
103 ThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrileTr 119
915 GCAGCAGATGAAGAAGTGGATGGCCCTGCGCTGCAGCCACCCAGG 964
119 pGlnGlnMetGluGlnLeuGlyMetAlaProAlaLeuGlnProThrGlnG 136
965 GTGCATGCGCGGCTTCCCTCTGCTTTCAGCGCGCGGAGGAGGGTC 1014
136 lYalaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyGlyVal 152
1015 CTAGTGTGCTCCCATCTGCAGAGCTTCTCGAGGTGTCGTACCGGTTCT 1064
153 LeuValAlaSerHisLeuGlnSerPheLeuGluValSerTyArgValle 169
1065 AGGCACCTTGGCCAGCCC 1083
169 uArgHisLeuAlaGlnPro 175
seq_name: US09680514.pep:US-09-680-514-40

```

```

seq_documentation_block:
; Sequence 40, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
;               Shiotsu, Yukimasa
;               Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-680-514-40

```

```

alignment_scores:
Quality: 819.00      Length: 371

```

```

Ratio: 3.357      Gaps: 14
Percent Similarity: 65.768      Percent Identity: 54.987
alignment_block:
us-09-680-514-6 x US-09-680-514-40
Align seg 1/1 to: US-09-680-514-40 from: 1. to: 332
64 AGCCCGGCTCCTCCTGCTGTGTGACCTCCGAGTCTCAGTAAACTGCTTCG 113
1 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
114 TGACTCCCATGTCTTCACAGCAGACTGAGCCAGTCCCGCAGAGTTCCACC 163
17 gaspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
164 CTTTGGCTACACCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 213
34 roleuProThrProValLeuLeuProAlaValAspPheSerLeuGlyglu 50
214 TGGAAAACCCAGATGGAGGAGACCAAGGACACAGACATCTTGGGAGCAG 263
51 TrpLysThrGlnMetGluGlnThrLysAlaGlnAspLeuGlyAlaVa 67
264 GACCCCTTCTGCTGGAGGAGTGTATGGCAGACCGGGACAACTGGGACCCA 313
67 lThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProt 84
314 CTTGCTCTCATCCCTCCTGGGCGAGCTTCTCGACAGGTCGCTCTCCTC 363
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTTGGGCGCTCGAGAGCTCTTGGAAACCCAGCTTCTCCTCCACAGGCGAG 413
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyAr 117
414 GACCACAGCTCACAGGATCCCAATGCCATCTTCTGAGCTTCCACACACC 463
117 gThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisL 134
464 TGCTCCGAGGAAAGTGCCTTCTCCTGATGCTGTAGGAGGTCACCCCTC 513
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
514 TCGCTCAGGGGTGGCGGTCTTGTGAGGTGGTTCGAGGGGGTTCAGAGC 563
151 CysValArg.....ArgAl 155
564 ACCAACAATATCGCGCTCGAGTCTACACAGAGCTTCTTTTAAAGCT 613
155 aProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuA 172
614 TAGACCAAGTGAGGAGATCCAGGGCGATGGCCAGCGCTCCAGGAGAAG 663
172 snGluLeuProAsnArgThrSerGly.....LeuLeuGluThrAsn 185
664 CTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGTGTCTGCTCG 713
186 PheThrAlaSerAlaArg.....ThrThrGl 194
714 ACACCTCTTGGGCATCCCTGGGCTCCC..... 741
194 ySerGlyLeu...LeuLysTrpGlnGlnGlyPheArgAlaLysIleProG 210
742 ..CTGAGCAGCTGCCCGCAGCAGGCGCTG...CAGCTGCAGGCTCTTG 786
210 lYLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeu 226
787 AGCCAACCTCATAGGCGCTTTTCTCTCTACACAGG.....GGCT 824
227 AsnArgIleHisGluLeuLeu..AsnGlyThrArgGlyLeuPheProGlyP 243
825 CCGCAGGCGCTTGGAGGAGTCTCCC..... 850

```



```
265 TCAGTGTCCAGAAATGCTGTGCTGCTCCCTGCTCCCTCCATCTGGGT 220
1
|||||:|
243 y.....CysLeuSerGlnLeuHisSerGly 251

seq_name: US09680514.pep:US-09-680-514-9

seq_documentation_block:
; Sequence 9, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
;           Shiotsu, Yukimasa
;           Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-680-514-9

alignment_scores:
Quality: 90.50 Length: 266
Ratio: 0.794 Gaps: 16
Percent Similarity: 42.857 Percent Identity: 27.820

alignment_block:
us-09-680-514-6/rev x US-09-680-514-9 ..
Align seg 1/1 to: US-09-680-514-9 from: 1 to: 365

874 TGTCAGAGGTGGGACCACTGCGGGGAGATCCCTCCAGGGCTGCAGG 825
|||||:|
50 CysProGluValHisPro.....LeuProThrProValle 61

824 AGCCCT.....GCTAGAGAAAGCCCGCTATGGAG 793
|||||:|
61 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 77

792 TTGCTCAAGCAGCGCTCCAGCTGCGGGCTGCTGGGCA..... 751
|||||:|
78 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 90
```

```
750 .....GCTGCTCAGGGAGCCCGAGGAT..... 727
|||||:|
90 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 107

726 .....GCCACAGAGGTGCCAGCAGCACACAGCTCCTCGGG 691
|||||:|
107 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 123

690 GTGGCACAGCTTGTAGTGGCACACAGCTT..... 661
|||||:|
124 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrTh 140

660 ....CTCCTGGAGCGTGGCCCTGCGCTGATCTTCCTCACTTGTCT 615
|||||:|
140 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 156

614 AAGCTTTTAAAGGAAGCTCTGTGTAGACTCGAGCGCGATATGTTGG 565
|||||:|
157 .....ArgGlyLysValArgPhe 162

564 .....TGCTCTAGAACCCCTCCGGAAC 542
|||||:|
163 LeuMetLeuValGlySerThrLeuCysValArg.....SerGlyG 177

541 CACCTCCAGAACCCCGCCCTGACGCGAGGCTGGA.....CCCT 501
|||||:|
177 yGlySerGlyGlySerGlyGlySerGlyGlyGlyArgAlaProt 194

500 CCTACAAGCATCAG.....GAAACGACCTT.....TCCTCGGAG 466
|||||:|
194 hrTyraArgAlaSerSerLeuProGlnSerPheLeuLeuLysSerLeuGlu 210

465 CAGGTGTTGGAAGCTCAGGAAGATGGCATTTGGGATCCTTGTGAGCTTGG 416
|||||:|
211 GlnValArgLysIleGlnGlyasp.....G 219

415 TCCTGCTGCTGTGGGAAGCTGGTTTCCAAGGAGGCTCTCAGGGCCCCA 366
|||||:|
219 yAlaAlaLeuGlnGluLysLeuCysAlaThrTyrrLysLeuCysHisPro 236

365 AGAGGAGAGCGACCTGTCCAGAAAGCTGCCCGAGGAGGATGAGAGGCA 316
|||||:|
236 lGluLeuValLeuLeuGlyHisSerLeu.....GlyIle 247

315 AGTGGGTCCAGTTGTCCCGCTGCTGCCATCACTCCCTCCAGCAGAAGG 266
|||||:|
248 ProTrpAlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaG 264

265 TCAGTGTCTCCAGAAATGCTGTGCTGCTGCTCTCTCTCTCTCTCTGGT 220
|||||:|
264 y.....CysLeuSerGlnLeuHisSerGly 272

seq_name: US09680514.pep:US-09-680-514-2

seq_documentation_block:
; Sequence 2, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
;           Shiotsu, Yukimasa
;           Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-680-514-2
```

alignment_scores:

```
Quality: 86.50 Length: 264
Ratio: 0.779 Gaps: 15
Percent Similarity: 42.045 Percent Identity: 28.409
```

alignment_block:

```
us-09-680-514-6/rev x us-09-680-514-2 ..
```

```
Align seg 1/1 to: US-09-680-514-2 from: 1 to: 340
```

```
874 TGTCAGGTGGGACCCAACTCGGGGAGATCCCTTCCAGGCGCTGCAGG 825
|||||:
29 CysProGluValHisPro.....LeuProThrProValLe 40
|||||:
824 AGCCCT.....GCTAGAGAAAGCCGCTATGAG 793
||| ||| |||: |||
40 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 56
|||||:
792 TTGGCTCAGCAGCCTGCCAGCTCGAGGCTGGCTGGGGCA..... 751
::: ||| |||: |||
57 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 69
|||||:
750 .....GCTGCTCGGGGAGCCAGGGAT..... 727
|||||: |||
69 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 86
|||||:
726 .....GCCAGAGAGTGTCCGAGCAGCAGCAGCTCTCGG 691
::: ||| |||: |||
86 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 102
|||||:
690 GTGCACAGCTTGTAGTGGGCACACAGCTT..... 661
::: ||| |||: |||
103 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 119
|||||:
660 ....CTCCTGAGCGCTGGCCATCGCCCTGGATCTTCTCCTCTCT 615
::: ||| |||: |||
119 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 135
|||||:
614 AAGCTTTTAAAGGAAGCTGTGGTAGACTCGAGCGCGCATATGTGG 565
|||||:
136 .....ArgGlyLysValArgPhe 141
|||||:
564 .....TGCTCTAGA..... 556
||| |||
```

```
142 LeuMetLeuValGlyGlySerThrLeuCysValArgGlyGlySerG1 158
555 .ACCCCTCCGGAACCACTCCAGAACCAGCCACCCCTGACGAGAGGTG 507
||||| |||: ||| |||:
158 yGlyGlySerGlyGlySerArgAlaProThrTyrArgAlaSerSerL 175
||||| |||: ||| |||:
506 GACCTCTCTACAAGCATCAGGAAGCGCACCTTCTCTCG...GAGCAGGTG 460
||| |||: ||| |||:
175 euPro.....GlnSerPheLeuLeuLysSerLeuGluGlnVal 187
||||| |||: ||| |||:
459 TTGNAAGCTCAGGAAGATGGCATTTGGGATCTCTGTGAGCTGTGGTCTGC 410
::: ||| ||| ||| |||
188 ArgLysIleGlnGlyAsp.....GlyAlaAl 196
||||| |||: ||| |||:
409 CTTGTGGAGGAAGCTGGCTTCCAAGGAGGCTGTGCAGGCGCCCAAGGAGG 360
||||| |||: ||| |||:
196 aLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluL 213
||||| |||: ||| |||:
359 AGACGACCTCTCCAGAAAGTGCCTCCAGGAGGATGAGAGGCAAGTGGG 310
::: |||: ||| ||| |||
213 euValLeuLeuGlyHisSerLeu.....GlyIleProTrp 224
||||| |||: ||| |||:
309 TCCAGTTGTCCCGCTGCTGCCATCCTCCAGCAGAGAGGCTCAGT 260
::: ||| ||| ||| |||
225 AlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly..... 239
||||| |||: ||| |||:
259 CTCCAGAAATGCTCTGCTTGGTCTCTCCATCTCGGT 220
|||||: ||| ||| |||
240 .....CysLeuSerGlnLeuHisSerGly 247

seq_name: US09680514.pep:US-09-680-514-7
seq_documentation_block:
; Sequence 7, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIVE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-680-514-7

alignment_scores:
  Quality: 86.50      Length: 264
  Ratio: 0.779       Gaps: 15
  Percent Similarity: 42.045      Percent Identity: 28.409

alignment_block:
us-09-680-514-6/rev x US-09-680-514-7  ..

Align seg 1/1 to: US-09-680-514-7 from: 1 to: 361

874 TGTCCAGGTGGACCAACTCGGGGAGATCCCTTCCAGGCGCTGCAGG 825
50 CysProGluValHisPro.....LeuProThrProValLe 61
824 AGCCCT.....GCTAGAGAAAGCCGCTATGGAG 793
61 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 77
792 TTGGCTCAAGCAGCTGCCAGCTCCAGGCGCTGGCTGGGCA..... 751
78 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 90
750 .....GCTGCTCAGGGAGCCCGAGGAT..... 727
90 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 107
726 .....GCCAGAGAGTCCGAGCAGCACCAGCTCCCTCGGG 691
107 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 123
690 GTGCACAGCTTGTAGTGGCAGCACACTT..... 661
124 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 140
660 ....CTCTGGAGCGCTCGCCCTCGGATCTTCTCTCACTTGTCT 615
140 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 156
614 AAGCTTTTAAAGAGAGCTCTGTGGTAGACTCGAGCGCGATATGTGG 565
157 .....ArgGlyLysValArgPhe 162
564 .....TGCTCTAGA..... 556
163 LeuMetLeuValGlyGlySerThrLeuCysValArgGlyGlySerGl 179
555 .ACCCCTCCGGAACCACTCCAGAACCCGCCCTGAGCAGAGGGTG 507
179 yGlyGlySerGlyGlySerArgAlaProThrTyrArgAlaSerSerL 196
506 GACCCCTCTACAGCATCAGGAACGACCTTCTCCCTCG...GAGCAGGTG 460
196 euPro.....GlnSerPheLeuLeuLysSerLeuGluGlnVal 208
459 TTGGAAGCTCAGGAAGATGGATCGTGTGAGCTGTGCTCTGC 410
209 ArgLysIleGlnGlyAsp.....GlyAlaAl 217
409 CCTGTGGAGGAAGTGGTTTCCAGGAGGCTCTGCAGGCGCCCAAGGAGG 360
217 aLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluL 234
359 AGACGGACCTGTCCAGAAAGCTGCCCGCAGGAGGATGAGAGCAAGTGGG 310
234 euValLeuLeuGlyHisSerLeu.....GlyIleProTrp 245
309 TCCAGTTGTCCCGCTGCTGCCATCACTCCCTCCAGCAGAGGGTCACTG 260
::: ||||| ||| :::::||||| |||
```

```
246 AlaProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGly..... 260
259 CTCCAGAAATGCTCTGTGCCTTGGTCTCTCCCTCATCTGGGT 220
261 .....CysLeuSerGlnLeuHisSerGly 268

seq_name: US09680514.pep:US-09-680-514-1

seq_documentation_block:
; Sequence 1, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd., 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-680-514-1

alignment_scores:
  Quality: 82.50      Length: 252
  Ratio: 0.743       Gaps: 14
  Percent Similarity: 44.048      Percent Identity: 28.175

alignment_block:
us-09-680-514-6/rev x US-09-680-514-1  ..

Align seg 1/1 to: US-09-680-514-1 from: 1 to: 328

874 TGTCCAGGTGGACCAACTCGGGGAGATCCCTTCCAGGCGCTGCAGG 825
29 CysProGluValHisPro.....LeuProThrProValLe 40
824 AGCCCT.....GCTAGAGAAAGCCGCTATGGAG 793
40 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 56
::: ||||| ||| :::::||||| |||
```

```
792 TTGGCTCAAGACGCTGCGCAGCTGCGAGGCGCTGGCTGGGGCA..... 751
      ::::: ||| ||| ::| |||||
57 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 69
      ::::: ||| ||| ::| |||||
750 .....GCTGCTCAGGGGAGCCAGGGAT..... 727
      |||||::: ||| ::|
69 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 86
      ::::: ||| ||| ::| |||||
725 .....GCCACAGAGTGTCCGAGCAGCACCAGCTCTCCGCG 691
      ::::: ||| ||| ::| |||||
86 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 102
      ::::: ||| ||| ::| |||||
690 GTGGCAGCAGCTGTAGTGGGCACACAGCTT..... 661
      ::| ||| ::| |||||
103 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 119
      ::::: ||| ||| ::| |||||
660 .....CTCCTGGAGCGCTGGCCATCGCCTGGATCTCTCACTGCTCT 615
      ::::: ||| ||| ::| |||||
119 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 135
      ::::: ||| ||| ::| |||||
614 AAGCTTTTAAAGGAAGCTCTGTGTAGACTCGAGGCGGATATGTTGG 565
      ||||| ::| ||| ::|
136 .....ArgGlyLysValArgPhe 141
      ||||| ::| ||| ::|
564 TGCTCTAGAACCCCTCCGGAAAC.....ACCTCCAGAACGCCACCC 521
      ::| ||||| ::| ||| ::|
142 LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProThrTy 158
      ::::: ||| ||| ::| |||||
520 TCACCGCAGAGGTGACCCCTCTCTACAGCATCAGGAACGACCTTCTCT 471
      ||||| ::| ||| ::|
158 rArgAlaSerLeuPro.....GlnSerPheLeuLeuLysS 171
      ||||| ::| ||| ::|
470 CG...GAGCAGGTGTGAAGCTCAGGAAGTGGCATTGGGATCCTGTG 424
      || ||||| ::| ||| |||
171 eLeuGluGlnValArgLysIleGlnGlyAsp..... 181
      || ||||| ::| ||| |||
423 AGCTGTGTCTCTCCCTCTGGAGGAGCTGGGTTCACAGGAGCTCTGCA 374
      || ||||| ::| ||||| ::|
182 .....GlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyLysLeuCy 196
      ::::: ||| ||| ::| |||||
373 GGGCCCCAAGGAGGAGCAGGACCTCTCCAGAAAGCTGCCCCAGGAGGAT 324
      ||||| ::| ||| ::|
196 sHisProGluGluLeuValLeuLeuGlyHisSerLeu..... 208
      ::::: ||| ||| ::| |||||
323 GAGAGGCAAGTGGTCCAGTGTCTCCCGTGTCTGCATCCTCCCTCCAG 274
      ::| ||||| ||| ::|
209 ..GlyIleProThrPheLeuSerCysProSerGlnAlaLeuGln 224
      ::::: ||| ||| ::| |||||
273 CAGAAAGGTCACTGCTCCAGAAATGCTGTGCTGTGCTCTCTCTCCATCT 224
      ||| ||||| ::| |||||
225 LeuAlaGly.....CysLeuSerGlnLeuHisSe 234
      ||||| ::| ||| ::|
223 GGGT 220
      |||
234 rGly 235
```

seq_name: US09680514.pep:US-09-680-514-5

seq_documentation_block:

; Sequence 5, Application US/09680514

; GENERAL INFORMATION:

; APPLICANT: Yokoi, Haruhiko

; Shiotsu, Yukimasa

; Konishi, Noboru

; TITLE OF INVENTION: NOVEL POLYPEPTIDES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 North Glebe Rd. 8th floor

; CITY: Arlington

; STATE: VA

; COUNTRY: USA

; ZIP: 22201-4741

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/680,514
FILING DATE: 06-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,337
FILING DATE: <Unknown>
APPLICATION NUMBER: JP P.HEI.7-102625
FILING DATE: 26-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 249-89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-680-514-5

alignment_scores:

Quality:	82.50	Length:	252
Ratio:	0.743	Gaps:	14
Percent Similarity:	44.048	Percent Identity:	28.175

alignment_block:

us-09-680-514-6/rev x US-09-680-514-5 ..

Align seg 1/1 to: US-09-680-514-5 from: 1 to: 349

```
874 TGTCGAAGTGGGACCAACTCGGGGAGATCCCTTCCAGGCGCTGCAGG 825
      |||||::| ||| ||| |||||
50 CysProGluValHisPro.....LeuProThrProValle 61
      ::::: ||| ||| ::| |||||
824 ACCCCCT.....GCTAGAGAAAAGCCCTATGCG 793
      ||| ||| ||| |||||
61 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 77
      ::::: ||| ||| ::| |||||
792 TTGGCTCAAGCAGCGCTGCCAGCTCGAGCGCCTGCTGGGGCA..... 751
      ::::: ||| ||| ::| |||||
78 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 90
      ::::: ||| ||| ::| |||||
750 .....GCTGCTCAGGGAGCCAGGGGAT..... 727
      |||||::: ||| ::|
90 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 107
      ::::: ||| ||| ::| |||||
726 .....GCCAGAGAGTGTCCGAGCAGCACCAGCTCTCCGCG 691
      ::::: ||| ||| ::| |||||
107 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 123
      ::::: ||| ||| ::| |||||
690 GTGGCAGCAGCTGTAGTGGGCACACAGCTT..... 661
      ::| ||| ::| |||||
124 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 140
      ::::: ||| ||| ::| |||||
660 .....CTCCTGGAGCGCTGGCCATCGCCTGGATCTCTCACTGCTCT 615
      ::::: ||| ||| ::| |||||
140 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 156
      ::::: ||| ||| ::| |||||
614 AAGCTTTTAAAGGAAGCTCTGTGTAGACTCGAGGCGGATATGTTGG 565
      ||||| ::| ||| ::|
157 .....ArgGlyLysValArgPhe 162
```

```
564 TGCTCTAGAACCCCTCGGAAC.....ACCTCCAGAACCGCCACCCC 521
    ::: :::::|||| ::::: |||
163 LeuMetLeuValGlySerThrLeuCysValArgAlaProThrTy 179
    ::::: |||
520 TGACCCAGAGGTCGACCTCTACAGCATCAGGAACGACCTTCCT 471
    |||::: |||
179 rArgAlaSerLeuPro.....GlnSerPheLeuLeuLysS 192
    |||::: |||
470 CG...GAGCAGGTGTGGAAGCTCAGGAAGATGGCATTGGGATCCTTGTG 424
    || ||||| |||
192 erLeuGlnValArgLysIleGlnGlyAsp..... 202
423 ACCTGTGCTCCTCCCTGTGAGGAAGCTGGTTCCAGAGGCTCTGCA 374
    ||| |||| ::||| |||
203 .....GlyAlaLeuGlnGlnLysLeuCysAlaThrTyLysLeuCy 217
373 GGGCCCCAAGAGGAGGACGACCTGTCCAGAAAGCTGCCCGCAGGAGGAT 324
    |||::: |||
217 sHisProGlnGluLeuValLeuLeuGlyHisSerLeu..... 229
323 GAGAGGCAAGTGGGTGCCAGTTGTCCCGTGTGCCATCCTCCCTCCAG 274
    :: ||||| |||
230 ..GlyIleProTrpAlaProLeuSerCysProSerGlnAlaLeuGln 245
273 CAGAAAGGTCACTGCTCCAGATGTCTGTGCTGTGCTGTGCTCCTCCATCT 224
    ||| |||||
246 LeuAlaGly.....CysLeuSerGlnLeuHis 255
223 GGGT 220
    |||
255 rGly 256
```

seq_name: US09680514.pep:US-09-680-514-24

seq_documentation_block:

; Sequence 24, Application US/09680514

; GENERAL INFORMATION:

; APPLICANT: Yokoi, Haruhiko

; Shiotsu, Yukimasa

; Konishi, Noboru

; TITLE OF INVENTION: NOVEL POLYPEPTIDES

; NUMBER OF SEQUENCES: 45

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHUYE P.C.

; STREET: 1100 North Glebe Rd. 8th floor

; CITY: Arlington

; STATE: VA

; COUNTRY: USA

; ZIP: 22201-4741

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/680,514

; FILING DATE: 06-Oct-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/765,337

; FILING DATE: <Unknown>

; APPLICATION NUMBER: JP P.HEI.7-102625

; FILING DATE: 26-APR-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Crawford, Arthur R.

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 249-89

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-816-4000

; TELEFAX: 703-816-4100

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-680-514-24

alignment_scores:
    Quality: 71.00      Length: 13
    Ratio: 5.462        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
us-09-680-514-6 x US-09-680-514-24 ..
Align seg 1/1 to: US-09-680-514-24 from: 1 to: 13
523 GGTGGCGGTCTCGAGGTGGTCCGGAGGGGTCTCTAGA 561
|||||
1 GlyGlyGlySerGlyGlySerGlyGlySerGlyGlySerArg 13
```

```
seq_documentation_block:
; Sequence 9, Application US/09680514
; GENERAL INFORMATION:
```

```

seq_documentation_block:
; Sequence 9, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741

```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/680,514

Sequence	Strd	ZScore	EScore	Len	Documentation
US09680514	pep:US-09-680-514-9	1857.00	953.49	2.0e-50	365
US09680514	pep:US-09-680-514-7	1813.00	931.93	3.6e-49	361
US09680514	pep:US-09-680-514-3	1765.00	899.74	8.4e-48	344
US09680514	pep:US-09-680-514-5	1751.00	896.49	2.1e-47	349
US09680514	pep:US-09-680-514-2	1721.00	884.28	1.5e-46	340
US09680514	pep:US-09-680-514-1	1659.00	852.75	9.0e-45	328
US09680514	pep:US-09-680-514-39	851.00	442.83	1.1e-21	175
US09680514	pep:US-09-680-514-40	817.00	421.59	9.2e-21	332
US09680514	pep:US-09-680-514-3	97.50	53.01	2.50	344
US09680514	pep:US-09-680-514-9	97.50	52.66	2.44	365
US09680514	pep:US-09-680-514-2	93.50	51.93	3.10	340
US09680514	pep:US-09-680-514-7	93.50	50.87	3.02	361
US09680514	pep:US-09-680-514-35	93.00	68.68	7.95	17
US09680514	pep:US-09-680-514-1	89.50	49.20	3.83	328
US09680514	pep:US-09-680-514-5	89.50	48.83	3.72	349
US09680514	pep:US-09-680-514-42	88.00	66.48	11.10	16
US09680514	pep:US-09-680-514-44	66.00	56.94	46.50	12
US09680514	pep:US-09-680-514-24	66.00	56.46	45.32	13
US09680514	pep:US-09-680-514-40	59.00	33.51	8.08	332
US09680514	pep:US-09-680-514-15	48.00	0.00	338.75	8
US09680514	pep:US-09-680-514-17	48.00	0.00	338.75	8
US09680514	pep:US-09-680-514-39	48.00	31.71	15.44	175
US09680514	pep:US-09-680-514-31	44.00	0.00	338.75	8
US09680514	pep:US-09-680-514-45	44.00	0.00	338.75	8
US09680514	pep:US-09-680-514-33	42.00	0.00	338.75	8
US09680514	pep:US-09-680-514-28	40.00	0.00	338.75	8
US09680514	pep:US-09-680-514-26	36.00	0.00	301.11	9
US09680514	pep:US-09-680-514-42	34.00	38.84	153.23	16
US09680514	pep:US-09-680-514-35	34.00	38.47	145.82	17
US09680514	pep:US-09-680-514-44	32.00	39.53	199.52	12
US09680514	pep:US-09-680-514-24	32.00	39.05	187.26	13
US09680514	pep:US-09-680-514-15	24.00	0.00	338.75	8
US09680514	pep:US-09-680-514-21	23.00	0.00	338.75	8
US09680514	pep:US-09-680-514-31	23.00	0.00	338.75	8
US09680514	pep:US-09-680-514-33	23.00	0.00	338.75	8
US09680514	pep:US-09-680-514-17	22.00	0.00	338.75	8
US09680514	pep:US-09-680-514-45	22.00	0.00	338.75	8
US09680514	pep:US-09-680-514-26	22.00	0.00	301.11	9
US09680514	pep:US-09-680-514-19	20.00	0.00	338.75	8
US09680514	pep:US-09-680-514-21	20.00	0.00	338.75	8
US09680514	pep:US-09-680-514-18	18.00	0.00	338.75	8
US09680514	pep:US-09-680-514-28	17.00	0.00	338.75	8

```

alignment_scores:
  Quality: 1857.00      Length: 365
  Ratio: 5.088          Gaps: 0
  Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
  us-09-680-514-8 x us-09-680-514-9      ..

Align seq 1/1 to: US-09-680-514-9 from: 1 to: 365

```

```

alignment_scores:
  Quality: 1857.00      Length: 365
  Ratio: 5.088          Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
  us-09-680-514-8 x us-09-680-514-9  ..

Align seg 1/1 to: US-09-680-514-9 from: 1 to: 365

1  ATGGAGCTGACTGAATTGCCTCTCGTGGTCATGCTTCTCCTAACTGCAAG  50
1  MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAla  17

51  GCTAACGCTGTCCAGCCCGGCTCCTCCTGCTGTGTGACCTCCGAGTCCTCA  100
17  gLeuThrLeuSerSerProAlaProProAlaCysAspLeuArgValLeuS  34

101  GTTAACTGCTTCTGACTCCCATGCTCTTCACAGCAGACTGAGCCAGTCC  150
34  erLyLeuLeuArgSpSerHisValLeuHisSerArgLeuSerGlnCys  50

151  CCAGAGGTTACACCTTTGGCTACACCTGTGCTCCTGCTGCCTGTGGACTT  200

```

```
51 ProGluValHisProLeuProLeuProThrProValLeuLeuProAlaValAsp 67
201 TAGCTTGGAGAAATGAAACCCAGATGGAGAGACCAAGCACAGACACA 250
67 eSerLeuGlyGluThrPlsThrGlnMetGluGluThrLysAlaGlnAspI 84
251 TTCCTGGAGCAGTACCCCTTCTGCTGGAGGAGTGTATGGCAGCAGCGGA 300
84 LeLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly 100
301 CAACCTGGACCCACTTCCCTCTCATCCCTCTGGGCGAGCTTCTGGACA 350
101 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyG 117
351 GGTCCGCTCTCTCTGGGCGCTGACAGACCTCTTGGAAACCCAGCTTC 400
117 nValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu 134
401 CTCACAGGCGAGGACACAGCTCACAAAGATCCCAATGCCATCTTCCTG 450
134 roProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu 150
451 AGCTTCCAACACCTGCTCCGAGGAAAGTCCGCTTCTGTAGTCTTAGG 500
151 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValG 167
501 AGGTCACACCTCTCGCTACGGTCCGGAGTGGCTCTGGCGGTGGTCTG 550
167 yGlySerThrLeuCysValArgSerGlyGlySerGlyGlyGlySerG 184
551 GTGCGGCTCCGGAGGCGGTGTCGCGCAACATATCCGCGCTCAGTCTTA 600
184 yGlyGlySerGlyGlyArgAlaProThrTyArgAlaSerSerLeu 200
601 CCACAGAGCTTCTTTAAAAGCTTAGACCAAGTGGAGAGATCCAGGG 650
201 ProGlnSerPheLeuLeuLysSerLeuGlnGlnValArgLysIleGln 217
651 CGATGGCGCAGCGCTCCAGAGAGTGTGTGCACCTACAAGCTGTGC 700
217 yAspGlyAlaAlaLeuGlnGlnLysLeuCysAlaThrTyLysLeuCy 234
701 ACCCGAGGAGCTGTGCTCTCGACACTCTCTGGGCATCCCTGGGCT 750
234 IsProGluGluLeuValLeuGlyHisSerLeuGlyLysProTrpAla 250
751 CCCCTGAGCAGTCCCGCCAGGCGCTCCAGCTGGCAGGCTGTGAG 800
251 ProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeu 267
801 CCAACTCATAGCGGCTTTTCTTACAGGGGCTCTGCAGGCGCTGG 850
267 rGlnLeuHisSerGlyLeuPheLeuTyGlnGlyLeuLeuGlnAlaLeu 284
851 AAGGGATCTCCCGAGTGGGTCCACCTTGGACACTGCAGCTGGAC 900
284 LuGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAsp 300
901 GTCCCGCACTTCCACCACTCTGGCAGCAGATGGAAGACTGGGAAT 950
301 ValAlaAspPheAlaThrIleTrpGlnGlnMetGluLeuGlyMe 317
951 GGCCCTGCGCTGAGCCCGGCTGATGGCGGCTCTGCGCTCTG 1000
317 tAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSer 334
1001 CTTTCCAGCGCGGAGGAGGGTCTAGTTGCCCTCCCATCTGCAGAGC 1050
334 LaPheGlnArgArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSer 350
1051 TTCCTGAGGTGCTGACCGCTTCTACGCCACCTTGGCCAGCCC 1095
351 PheLeuGluValSerTyArgValLeuArgHisLeuAlaGlnPro 365
```

```
seq_name: US09680514.pep:US-09-680-514-7
seq_documentation_block:
; Sequence 7, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotzu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; LENGTH: 361 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-680-514-7

alignment_scores:
Quality: 1813.00 Length: 365
Ratio: 5.022 Gaps: 2
Percent Similarity: 98.904 Percent Identity: 98.904

alignment_block:
us-09-680-514-8 x us-09-680-514-7
Align seg 1/1 to: US-09-680-514-7 from: 1 to: 361
1 ATGGAGCTGACTGAATGCTCTCGTGGTCATGCTTCTCTACTGCAAG 50
1 MetGluLeuThrGluLeuLeuValValMetLeuLeuThrAlaAr 17
51 GCTAAGCGTGTCCAGCCGGCTCTCTGCTGTGTGACCTCCGAGTCTCA 100
17 gLeuThrLeuSerSerProAlaProProAlaCysAspLeuArgValLeuS 34
101 GTAAACTGCTTCGTGACTCCCATGCTTTCACAGCAGACTGAGCCAGTGC 150
34 erLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys 50
151 CCAGAGGTTCACCCCTTGGCTACACCTGTCTGCTGCTGCTGCTGCTG 200
```



```

51 ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPh 67
201 TAGCTTGGAGATGGAACCCAGATGGAGGACCAAGGCACAGGACA 250
    |||
67 eSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspI 84
    |||
251 TTCTGGGAGCAGTCACCTTCTGCTGGAGGAGTGTGGCAGCAGCGGA 300
    |||
84 leLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaAlaArgGly 100
    |||
301 CAATGGGACCCACTTCCCTCTATCTCTCTCTCTCTCTCTCTCTCTG 350
    |||
101 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyI 117
    |||
351 GGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 400
    |||
117 nValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeu 134
    |||
401 CTCCACAGGCGAGGACACAGCTCACAGGATCCCAATGCCATCTTCT 450
    |||
134 roProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu 150
    |||
451 AGCTTCCAACACCTGCTCCGAGGAAAGTGGCTTCTCTCTCTCTCT 500
    |||
151 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValG 167
    |||
501 AGGTCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 550
    |||
167 yGlySerThrLeuCysValarg...GlyGlyGlySerGlyGlySerG 183
    |||
551 GTGCGGCTCGGAGGCGGTGTCGCGCAACATATCGCGCTCGAGTCTA 600
    |||
183 lyGlyGlySer.....ArgAlaProThrTyrArgAlaSerSerLeu 196
    |||
601 CCACAGAGCTCTCTTTAAAGCTTACAGCAAGTGGAGGATCCAGGG 650
    |||
197 ProGlnSerPheLeuLeuLysSerLeuGlnValArgLysIleGlnG 213
    |||
651 CGATGGCGCAGCGCTCCAGGAGAGCTGTGTGCCACCTACAAGCTGTGC 700
    |||
213 yAspGlyAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysH 230
    |||
701 ACCCGAGGAGCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 750
    |||
230 isProGluGluValLeuLeuGlyHisSerLeuGlyIleProTrpAla 246
    |||
751 CCCCTGAGCAGCTGCCCGCAGCGGCTCGAGCTGGCAGCTCTCTTG 800
    |||
247 ProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeu 263
    |||
801 CCAACTCCATAGCGGCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT 850
    |||
263 rGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeu 280
    |||
851 AAGGATCTCCCGGAGTTGGTCCCACTTGGACACACTGCAGCTGGAC 900
    |||
280 luGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAsp 296
    |||
901 GTCCCGCACTTTCACCACTCTGGCAGCAGATGGAAGACTGGGAAT 950
    |||
297 ValAlaAspPheAlaThrIleTrpGlnGlnMetGluLeuGlyMe 313
    |||
951 GGCCCTCTCCCTGAGCCCAAGGAGGCTGCTCTCTCTCTCTCTCTCT 1000
    |||
313 tAlaProAlaLeuGlnProThrGlnGlyAlaMetProAlaPheAlaSer 330
    |||
1001 CTTTCCAGCGCGGAGGAGGCTCTCTCTCTCTCTCTCTCTCTCTCT 1050
    |||
330 laPheGlnArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSer 346
    |||
1051 TTCTTGAGGTGTCGTACCGCGTCTACGCGACCTTCTCCCGAGGCC 1095
    |||
347 PheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro 361
    |||

```

```

seq_name: US09680514.pep:US-09-680-514-3
seq_documentation_block:
; Sequence 3, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 344 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-680-514-3

alignment_scores:
Quality: 1765.00 Length: 344
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
us-09-680-514-8 x US-09-680-514-3 ..
Align seg 1/1 to: US-09-680-514-3 from: 1 to: 344

64 AGCCCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 113
    |||
1 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
    |||
114 TGACTCCCATGTCTTTCACAGCAGACTGAGCCAGTGCCTGAGGTTTACC 163
    |||
17 gAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
    |||
164 CTTTGGCTACACCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 213
    |||
34 roLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
    |||
214 TGGAAACCACAGATGGAGGAGACCAAGGCACAGACATTTCTGGAGCAGT 263
    |||

```

```
|||||
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
264 GACCCCTCTCTGTGGAGGAGTGTGGAGCAGCGGGACAACCTGGGACCA 313
67 lThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyPro 84
314 CTGCTCTCATCCCTCTCTGGGGAGCTTTCTGGACAGGTCCTCTCTC 363
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTGGGGCCCTGCAGAGCTCTTGGAAACCCAGCTTCTCCACAGGCGAG 413
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
414 GACCACAGCTCACAGGATCCATGATCCATCTCTCTGAGCTTCCACACC 463
117 gThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisL 134
464 TGCTCCGAGGAAAGGTGCGTTTCTGATGCTTGTAGGAGGTCACCCCTC 513
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
514 TCGGTACGTCGGAGGTGGCTCTGGCGGTGTGTGGTGGCGGCTCCGG 563
151 CysValArgSerGlyGlySerGlyGlySerGlyGlySerGlyGlySerG 167
564 AGCGGTGCTGCGCAACATATCGCGCTCGAGTCTACACAGAGCTTCC 613
167 yGlyGlyArgAlaProThrTyrArgAlaSerSerLeuProGlnSerPheL 184
614 TTTTAAAAAGCTTAGACAAGTGGAGGATCCAGGCGGATGCGGAGCG 663
184 euLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaLa 200
664 CTCAGAGAAAGCTGTGTGCACCTACAAGCTGTGCCACCCCGAGAGCT 713
201 LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGlu 217
714 GGTGCTGCTCGACACACTCTGGGCATCCCTGGCTCCCTCAGCAGCT 763
217 uValLeuLeuGlyHisSerLeuGlyIleProThrAlaProLeuSerSerC 234
764 GCGCCAGCCAGGCGCTCAGCTGCGAGGCTGCTGAGCCCAACTCCATAGC 813
234 ysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSer 250
814 GGCCTTTTCTCTACAGGGGCTCTCGAGGCTTGAAGGATCTCCCC 863
251 GlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerPr 267
864 CGAGTTGGTCCCACCTTGGACACACTGACGCTGGAGCTGGCGGACTTTG 913
267 oGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheA 284
914 CCACCAACATCTGGACAGATGGAAGAACTGGGAATGGCCCTGCGCTG 963
284 laThrThrIleTrpGlnMetGluGluLeuGlyMetAlaProAlaLeu 300
964 CAGCCCAACCCAGGTGGCATCGCGGCTTGGCTCTGCTTTCAGGCGCG 1013
301 GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgAr 317
1014 GCGAGGAGGCTCTAGTTCCTCCATCTGCAGAGCTTCTCTGAGGTGT 1063
317 gAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValS 334
1064 CGTACCGGCTTCTACGCCACCTTGGCCAGGCC 1095
334 erTyrArgValLeuArgHisLeuAlaGlnPro 344
seq_name: US09680514.pep:US-09-680-514-5
```

```
seq_documentation_block:
; Sequence 5, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
;               Shiotsu, Yukimasa
;               Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-680-514-5

alignment_scores:
Quality: 1751.00 Length: 365
Ratio: 5.017 Gaps: 1
Percent Similarity: 95.616 Percent Identity: 95.616

alignment_block:
us-09-680-514-8 x US-09-680-514-5 ...
Align seg 1/1 to: US-09-680-514-5 from: 1 to: 349
1 ATGGAGCTGACTGAATTGCTCTCGTGGTCATGCTTCTCTTAACCTCAAG 50
|||||
1 MetGluLeuThrGluLeuLeuValMetLeuLeuThrAlaAr 17
51 GCTAAGCTGTCCAGCCCGGCTCTCTCTGTGACCTCCGAGTCTCA 100
|||||
17 gLeuThrLeuSerSerProAlaProAlaCysAspLeuArgValLeuS 34
101 GTAACCTGCTCTGTGACTCCCATGCTTTCACAGCAGACTGAGCCAGTGC 150
|||||
34 erLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCys 50
151 CCAGAGGTTTACCCCTTGTGCTACACCTGTCTGCTGCTGCTGCTGACTT 200
|||||
51 ProGluValHisProLeuProThrProValLeuLeuProAlaValAspPh 67
201 TAGCTTGGGAGAAATGGAAAAACCCAGATGGAGGAGACCAAGGCACAGCA 250
```

```
|||||
67 eSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspI 84
|||||
251 TTCTGGGAGCAGTGACCTTCTGCTGGAGGAGTGATGCGCAGCGGGGA 300
|||||
84 leLeuGlyAlaValThrLeuLeuLeuGluGlyValMetAlaIaArgGly 100
|||||
301 CAACTGGGACCCACTGCTCTCATCCCTCCTGGGCGAGCTTCTTGACA 350
|||||
101 GlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGI 117
|||||
351 GGTGGCTCTCTCTGGGGCCCTGCAGAGCTCTTGGACCCAGCTTC 400
|||||
117 nValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuP 134
|||||
401 CTCACAGGCGAGGACCACTGCTCACAAGGATCCCAATGCCATCTTCGT 450
|||||
134 roProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeu 150
|||||
451 AGCTTCCAAACACTGCTCCGAGGAAGTGCCTTCTGATGCTGTAGG 500
|||||
151 SerPheGlnHisLeuLeuArgGlyLysValArgPheLeuMetLeuValGI 167
|||||
501 AGGTCCACCTCTGCTGACGTCCGGAGTGGCTCTGGCGGTGTTCTG 550
|||||
167 yGlySerThrLeuCysValArg..... 174
|||||
551 GTGGCGGCTCGGAGCGCTGCTGGCGCAACATATCGGCGCTCGAGTCTA 600
|||||
175 .....ArgAlaProThrTyrArgAlaSerSerLeu 184
|||||
601 CCACAGAGCTTCCTTTTAAAGCTTAGAGCAAGTGAGGAATCCAGGG 650
|||||
185 ProGlnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGI 201
|||||
651 CGATGGCGCAGCTCCAGGAGAGCTGTGTGCCACCTACAGCTGTGCC 700
|||||
201 yAspGlyAlaAlaLeuGlnGluLysLeuCysAlaThrTyrLysLeuCysH 218
|||||
701 ACCCGAGGAGCTGGTGTCTCGGACACTCTCTGGGCATCCCTGGGCT 750
|||||
218 isProGluGluLeuValLeuLeuGlyHisSerLeuGlyIleProTrpAla 234
|||||
751 CCCCTGACAGCTGCCACCATCTCGAGGCCCTGCAGCTGGCAGCTGTTG 800
|||||
235 ProLeuSerSerCysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSe 251
|||||
801 CCAACTCCATAGCGGCTTTCTCTTACCAGGGCTCTGCAGGCCCTGG 850
|||||
251 rGlnLeuHisSerGlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuG 268
|||||
851 AAGGATCTCCCGAGTGGGTCCACCTTGGACACACTCAGCTGGAC 900
|||||
268 luGlyIleSerProGluLeuGlyProThrLeuAspThrLeuGlnLeuAsp 284
|||||
901 GTCGCCGACTTTGCCACCATCTGGCAGCAGATGGAAGAACTGGGAAT 950
|||||
285 ValAlaAspPheAlaThrThrIleTrpGlnGlnMetGluGluLeuGlyMe 301
|||||
951 GGCCCTGCTGAGCCACCCAGGAGGTCATGCCGGCCTTGCCTGCTG 1000
|||||
301 tAlaProAlaLeuGlnProThrGlnGlnGlyAlaMetProAlaPheAlaSer 318
|||||
1001 CTTTCCAGCGCGGCGAGGAGGCTCTAGTTGCTCCCATCTCAGAGC 1050
|||||
318 laPheGlnArgAlaGlyGlyValLeuValAlaSerHisLeuGlnSer 334
|||||
1051 TTCCTGGAGGTGCTGCTACCGGTTCTAGCCACCTTGGCCAGCC 1095
|||||
335 PheLeuGluValSerTyrArgValLeuArgHisLeuAlaGlnPro 349
|||||
```

seq_name: US09680514.pep:US-09-680-514-2

```
seq_documentation_block:
: Sequence 2, Application US/09680514
: GENERAL INFORMATION:
: APPLICANT: Yokoi, Haruhiko
: Shiotsu, Yukimasa
: Konishi, Noboru
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERHVE P.C.
: STREET: 1100 North Glebe Rd. 8th floor
: CITY: Arlington
: STATE: VA
: COUNTRY: USA
: ZIP: 22201-4741
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/680,514
: FILING DATE: 06-Oct-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/765,337
: FILING DATE: <Unknown>
: APPLICATION NUMBER: JP P.HEI.7-102625
: FILING DATE: 26-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Crawford, Arthur R.
: REGISTRATION NUMBER: 25,327
: REFERENCE/DOCKET NUMBER: 249-89
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-816-4000
: TELEFAX: 703-816-4100
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 340 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-680-514-2

alignment_scores:
Quality: 1721.00 Length: 344
Ratio: 5.062 Gaps: 2
Percent Similarity: 98.837 Percent Identity: 98.837

alignment_block:
us-09-680-514-8 x US-09-680-514-2 ..
Align seg 1/1 to: US-09-680-514-2 from: 1 to: 340
64 AGCCGGCTCCTCTGCTGTGACCTCGAGCTCCTCAGTAACTGCTTCG 113
|||||
1 SerProAlaProProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
|||||
114 TGACTCCCATGCTCTCACAGCAGACTGAGCCAGTGCCCGAGGTTCA 163
|||||
17 gAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
|||||
164 CTTTGCCTTACACTGCTCTGCTGCTGCTGTGGACTTTAGTTGGAGAA 213
|||||
34 roLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
|||||
214 TGGAAACCCAGATGGAGGAGACCAAGCCAGCAGCATTTCTGGGAGCAGT 263
|||||
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
|||||
```

```
264 GACCTTCTGCTGGAGGAGTGTGTCAGCAGCGGGGACAACTGGGACCCA 313
67 lThrLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProT 84
314 CTTGCCCTCATCCTCTCTGGGAGCTTTCTGGACAGGTCGCTCCTC 363
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTTGGGGCCCTGCAGAGCTCTTGGAAACCCAGCTTCTCCACAGGSCAG 413
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
414 GACCACAGCTCACAAAGATCCCAATGCCATCTTCTGAGCTTCCAACACC 463
117 gThrThraAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisL 134
464 TGCCTCCAGGAAAGGTGCTTCTGATGCTTGTAGGAGGCTCACCTC 513
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
514 TCGGTACGGTCCGGAGGTGGCTCTGGCGGTGGTCTGCTGGCGGCTCCGG 563
151 CysValArg...GlyGlyGlySerGlyGlyGlySerGlyGlySer.. 165
564 AGCGGTGTCGCGCAACATATCGCGCTCGAGTCTACACAGAGCTTCC 613
166 .....ArgAlaProThrTyArgAlaSerSerLeuProGlnSerPheL 180
614 TTTTAAAGCTTAGACAGTGGAGGAGATCCAGGCGGATGCGCAGCG 663
180 euLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla 196
664 CTCAGGAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCT 713
197 LeuGlnGluLysLeuCysAlaThrTyLysLeuCysHisProGluGluLe 213
714 GGTGTCGTCGACACTCTCTGGGCATCCCTCGGCTCCCTCAGCAGCT 763
213 uValLeuLeuGlyHisSerLeuGlyIleProTTPAlaProLeuSerSerC 230
764 CCCCAGCAGCGCCCTGCAGCTGGCAGCTGCTTGAAGCAACTCCATAGC 813
230 ysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSer 246
814 GGCCTTTCTCTACAGGGGCTCTGCAGGCGCTTGAAGGATCTCCCC 863
247 GlyLeuPheLeuTyGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerPr 263
864 CGAGTTGGTCCCACTTGGACACTGTCAGCTGGAGCTGCCGACTTGG 913
263 oGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheA 280
914 CCACCACCATCTGCAGCAGATGAAGAACTGGGAATGGCCCTGCCCTG 963
280 laThrThrIleTrpGlnGlnMetGluGluGlyMetAlaProAlaLeu 296
964 CAGCCCCACCCAGGTGCATCCCGGCTCTGCCTCTGCTTTCAGGCGCG 1013
297 GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgAr 313
1014 GCGAGGAGGCTCTAGTTGCTCCCATCTGCAGAGCTTCTCGAGGTGT 1063
313 gAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValS 330
1064 CGTACCGGTTCTACGCACCTCTCCCGAGGCC 1095
330 erTyArgValLeuArgHisLeuAlaGlnPro 340
```

seq_name: US09680514.pep:US-09-680-514-1

seq_documentation_block:

; Sequence 1, Application US/09680514

; GENERAL INFORMATION:

```
APPLICANT: Yokoi, Haruhiko
Shiotzu, Yukimasa
Konishi, Noboru
TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 North Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/680,514
FILING DATE: 06-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,337
FILING DATE: <Unknown>
APPLICATION NUMBER: JP P.HEI.7-102625
FILING DATE: 26-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 249-89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-680-514-1
```

alignment_scores:

Quality:	1659.00	Length:	344
Ratio:	5.058	Gaps:	1
Percent Similarity:	95.349	Percent Identity:	95.349

alignment_block:

us-09-680-514-8 x US-09-680-514-1 . . .

Align seg 1/1 to: US-09-680-514-1 from: 1 to: 328

```
64 AGCCCGGCTCCTCCTCTGTGTGACCTCCGAGTCTCAGTAACTGCTTCG 113
1 SerProAlaProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
114 TGACTCCCATGTCTTCACAGCAGACTGAGCCAGTGCACAGAGGTTCCACC 163
17 gapSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
164 CTTTGCCTACACTGTCTGCTGCTCCTCTGTGGACTTTAGCTTGGGAGAA 213
34 roLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
214 TGGAAACCCAGATGGAGAGACCAAGGACACAGCATTTCTGGAGCAGT 263
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
264 GACCCCTTCTGTGGAGGAGTGTATGTCAGCAGCGGGGACAACTGGGACCCA 313
67 lThrLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProT 84
```

```
314 CTGCTCTCATCCCTCTCTGGGGAGCTTTCTGGACAGGTCCGCTCTCTC 363
      |||
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTGCGGCGCTGCAGAGCTCTTGGACACCGCTTCTCCACAGGCGAG 413
      |||
101 LeuGlyAlaLeuGlnSerLeuGlyThrGlnLeuProGlnGlyAr 117
414 GACCACAGCTCACAGGATCCCAATGCCATCTCTGAGCTTCCAACACC 463
      |||
117 gThrThralahisylaspproasnAlailepLeuSerPheGlnHisL 134
464 TGCTCCGAGGAAAGTGGTTCCTGATGCTGTAGGAGGCTCCACCCCTC 513
      |||
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlySerThrLeu 150
514 TGCCTACGGTCCGAGGAGTGGCTCTGGCGGTGGTCTGGTGGCGGCTCGG 563
      |||
151 CysValArg..... 153
564 AGCGGGTCTGCGCGCAACATATCGCGCTCGAGTCTACACAGAGCTTCC 613
      |||
154 .....ArgAlaProThrThrArgAlaSerSerLeuProGlnSerPheL 168
614 TTTTAAAGCTTAGACAAGTGAAGAGATCCAGGCGGATGGCGCAGCG 663
      |||
168 euLeuLysSerLeuGluGlnValArgLysIleGlnGlyAspGlyAlaAla 184
664 CTCAGGAGAGCTGTGTGCCACCTACAGCTGTGCCACCCCGAGGAGCT 713
      |||
185 LeuGlnGluLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLe 201
714 GGTGCTGCTCGCACACTCTCTGGGCATCCCTGGGCTCCCTCGAGCAGCT 763
      |||
201 uValLeuLeuGlyHisSerLeuGlyIleProTrpAlaProLeuSerSerC 218
764 GCGCCAGCCAGCGCTCTGAGTGGCAGGCTGTTGAGCCAACTCCATAGC 813
      |||
218 ysProSerGlnAlaLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSer 234
814 GCGCTTTCTCTACAGGGGCTCTGAGGCGCTTGAAGGATCTCCCG 863
      |||
235 GlyLeuPheLeuTyrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerPr 251
864 CGAGTTGGTCCCGCTGGACACTGCAGCTGCAGCTGCAGCTGCAGCTTG 913
      |||
251 oGluLeuGlyProThrLeuAspThrLeuGlnLeuAspValAlaAspPheA 268
914 CCACCACCATCTGCAGCAGATGGAAGAACTGGGAATGGCCCTCGCCTG 963
      |||
268 laThrThrIleTrpGlnMetGluGluLeuGlyMetAlaProAlaLeu 284
964 CAGCCACCCAGGTCGATCGCGGCTCTGCGCTCTGCTTTCAGCGCGG 1013
      |||
285 GlnProThrGlnGlyAlaMetProAlaPheAlaSerAlaPheGlnArgAr 301
1014 GCGAGGAGGGTCTCTAGTTGGCTCCCATCTGCAGAGCTTCTCTGGAGTGT 1063
      |||
301 gAlaGlyGlyValLeuValAlaSerHisLeuGlnSerPheLeuGluValS 318
1064 CGTACCGGTTCTACGCCACCTTCCCGAGGCC 1095
      |||
318 erTyrArgValLeuArgHisLeuAlaGlnPro 328
```

seq_name: US09680514.pep:US-09-680-514-39

seq_documentation_block:

; Sequence 39, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotzu, Yukimasa
; Konishi, Noboru

TITLE OF INVENTION: NOVEL POLYPEPTIDES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 North Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/680,514
FILING DATE: 06-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/765,337
FILING DATE: <Unknown>
APPLICATION NUMBER: JP P.HEI.7-102625
FILING DATE: 26-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Crawford, Arthur R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 249-89
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-680-514-39

alignment_scores:
Quality: 851.00 Length: 173
Ratio: 5.065 Gaps: 0
Percent Similarity: 97.110 Percent Identity: 97.110
alignment_block:
us-09-680-514-8 x us-09-680-514-39 ..

Align seg 1/1 to: US-09-680-514-39 from: 1 to: 175
577 CCAACATATCGCGCTCGAGTCTACACAGAGCTTCCTTTTAAAGGCTT 626
||| |||
3 ProLeuGlyProAlaSerSerLeuProGlnSerPheLeuLeuLysCysLe 19
627 AGAGCAAGTAGGAGATCCAGGGCGATGGCGCAGCGCTCCAGGAGAAC 676
||| |||
19 uGluGlnValArgLysIleGlnGlyAspGlyAlaAlaLeuGlnGluLysL 36
677 TGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGTCTCGGAG 726
||| |||
36 euCysAlaThrTyrLysLeuCysHisProGluGlyLeuValLeuGly 52
727 CACTCTCTGGGCATCCCTGGGCTCCCTGAGCAGCTGCCCGACCGAGGC 776
||| |||
53 HisSerLeuGlyIleProTrpAlaProLeuSerSerCysProSerGlnAl 69
777 CCTGCAGCTGGCAGGCTGCTGTAGCCAACTCCATAGCGGCTTTTCCTCT 826
||| |||
69 aLeuGlnLeuAlaGlyCysLeuSerGlnLeuHisSerGlyLeuPheLeu 86
827 ACCAGGGCTCTTCAGCGGCTTGAAGGGATCTCCCCCGAGTTGGGTCCC 876
||| |||

```

86 yrGlnGlyLeuLeuGlnAlaLeuGluGlyIleSerProGluLeuGlyPro 102
877 ACCTTGGACACACTGCAGCTGCAGCTCGCGACTTTGCCACCACTCTG 926
|||||
103 ThrLeuAspThrLeuGlnLeuAspValAlaAspPheAlaThrThrIleTr 119
|||||
927 GCAGCAGATGGAAGAACTGGGAATGGCCCTCGCCTCCAGCCCACTCCAGG 976
|||||
119 pGlnGlnMetGluGluLeuGlyMetAlaProAlaLeuGlnProThrGlnG 136
977 GTGCCATCGCGGCTCGCTCTGCTTCCAGCCCGGCGAGAGGGTC 1026
|||||
136 IyAlaMetProAlaPheAlaSerAlaPheGlnArgArgAlaGlyVal 152
|||||
1027 CTAGTTGCTCCCATCTCCAGCTTCTCTGGAGGTGCTGACGCGTTCT 1076
|||||
153 LeuValAlaSerHisLeuGlnSerPheLeuGluValSerIyrArgVal 169
1077 AGCCACCTTCCCGAGCCC 1095
169 uArgHisLeuAlaGlnPro 175

```

seq_name: US09680514.pep:US-09-680-514-40

```

seq_documentation_block:
; Sequence 40, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
;               Shiotsu, Yukimasa
;               Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-680-514-40

```

alignment_scores: Quality: 817.00 Length: 375

```

Ratio: 3.348 Gaps: 14
Percent Similarity: 65.067 Percent Identity: 54.400
alignment_block:
us-09-680-514-8 x US-09-680-514-40 ..
Align seg 1/1 to: US-09-680-514-40 from: 1 to: 332
64 AGCCCGGCTCCTCCTCTGCTGCTGACCTCCGAGTCTCAGTAAACTGCTTCG 113
1 SerProAlaProAlaCysAspLeuArgValLeuSerLysLeuLeuAr 17
114 TGACTCCCATGTCTTTCACAGCAGACTGAGCCAGTGCACAGAGTTCCACC 163
17 gAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisP 34
164 CTTTGGCTACACCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213
34 roLeuProThrProValLeuLeuProAlaValAspPheSerLeuGlyGlu 50
214 TGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTTCTGGGAGCAGT 263
51 TrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaVa 67
264 GACCTTCTCTGCTGGAGGAGTGTATGGCAGCAGCGGGGACAACTGGGACCA 313
67 lThrLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProT 84
314 CTTGCTCTCATCCTCCTGCGGCGAGCTTTCTGGACAGGTCCTGCTCCTC 363
84 hrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu 100
364 CTTGGGCGCTCGAGAGCTCCTTGGAAACCCAGCTTCTCCACAGGCGAG 413
101 LeuGlyAlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyAr 117
414 GACCACAGTTCACAAGATCCCAATGCCATCTTCTCCTGAGTTCACAACACC 463
117 gThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisL 134
464 TGCTCCGAGGAAAGGTCCGTTTCTGATGCTTGTAGGAGGTCACCCCTC 513
134 euLeuArgGlyLysValArgPheLeuMetLeuValGlyGlySerThrLeu 150
514 TGGCTACGTTCCGGAGGTGCTCTGCGCGTGTCTGCTGGCGGCTCCGG 563
151 CysValArg..... 153
564 AGCGGTCTGCTGCGCCCAACATATCGCGCTCGAGTCTTACCACAGAGCTTCC 613
154 .....ArgAlaProProThrThrAlaValProSerArgThrSerLeuV 168
614 TTTTAAAGCTTAGAGCAGTGTAGGAGATCCAGGCGGATGCGGCGAGCG 663
168 alLeuThrLeuAsnGluLeuProAsnArgThrSerGly.....Leu 181
664 CTCAGGAGAAGCTGTGTGCCACTTACAAGCTGTGCCACCCCGAGGAGCT 713
182 LeuGluThrAsnPheThrAlaSerAlaArg..... 191
714 GGTGCTGCTCGGACACTCTCTGGGCATCCCTCGGCTCC..... 753
192 ....ThrThrGlySerGlyLeu...LeuLysTrpGlnGlnGlyPheArgA 206
754 .....CTGAGCAGCTGCCCGCCAGCCAGCCCTG...CAGCTG 786
206 laLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIle 222
787 GCAGGCTGCTTGAGCCAACCTCCCATAGCGGCTTTTCTCTTACCAGG... 832
223 ProGlyTyrIleAsnArgIleHisGluLeuLeu.AsnglyThrArgGlyL 239
833 .....GGCTCTCGAGGCGCTGGAAGGATCTCCC..... 862

```

```

US-09-680-514-3

alignment_scores:
  Quality: 97.50      Length: 264
  Ratio: 0.841        Gaps: 14
  Percent Similarity: 43.939    Percent Identity: 27.273

alignment_block:
us-09-680-514-8/rev x US-09-680-514-3      ..

Align seg 1/1 to: US-09-680-514-3 from: 1 to: 344

886  TGTCCAAGTGGGACCACTCGGGGAGATCCCTTCACGGGCTCCAGG 837
|||||::: ||| ||||| |||:::
29  CysProGluValHisPro.....LeuProThrProValle 40

836  AGCCCTT.....GCTAGAGAAAGCCGCTATGGAG 805
||| ||| ||| |||::: |||||
40  uLeuProAlaValAspPheSerLeuGly_GluTriPlysThrGlnMetGlu 56

804  TTGGCTCAACGAGCTGCCAGCTCGAGGCCCTGGCTGGGGCA..... 763
:::||||| ||| ::| |||||
57  GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 69

762  ..GCTGCTCAGGGGAGCCCGGGAT..... 739

```

```
seq_documentation_block:
; Sequence 3, Application US/09680514
```

```
seq_documentation_block;  
; Sequence 3, Application US/09680514  
; GENERAL INFORMATION:
```

APPLICANT: Yokoi, Haruhiko

Shiotsu, Yukimasa

; Konishi, Noboru

; TITLE OF INVENTION: NOVEL PO

; NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VAND

STREET: 1100 North Glebe

CITY: Arlington
COUNTY: York

STATE: VA
COUNTRY: USA

COUNTRY: USA
ZIP: 22201-4741

; ZIP: 22201-4741
; COMPUTER READABLE FORM.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compat
MEDIUM TYPE: Floppy dis

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS

OPERATING SYSTEM: PC-DOS
SOFTWARE: PatentIn Release 1.0

```

; ;
; SOFWAKE: FACE/CPU RETE
; ;
; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/

FILING DATE: 06-Oct-2000

CLASSIFICATION: <Unknown>

;
;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/

; FILING DATE: <Unknown>

APPLICATION NUMBER: JP

FILING DATE: 26-APR-1999

ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur

REGISTRATION NUMBER: 25

REFERENCE/DOCKET NUMBER

TELECOMMUNICATION INFORMATION
TELEPHONE: 703-836-4000

TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100

TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 3.

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids

```

      , 344 AMINO ACIDS
      :
      TYPE: amino acid

```

FILE: AMINO ACID
STRANDEDNESS: <Unknown>

```

; STRAIGHTNESS: <UNKNOWN>
; TOPOLOGY: linear
;

```

MOLECULE TYPE: peptide

```

; PROJECT FILE: PEPAGE
; SEQUENCE DESCRIPTION: SEQ ID

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84


```
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-680-514-7

alignment_scores:
    Quality: 93.50      Length: 261
    Ratio: 0.813        Gaps: 15
    Percent Similarity: 44.061      Percent Identity: 27.969

alignment_block:
us-09-680-514-8/rev x US-09-680-514-7 ..

Align seg 1/1 to: US-09-680-514-7 from: 1 to: 361

886 TGTCAAGTGGGACCAACTCGGGGAGATCCCTTCAGGCGCTGCAGG 837
|||||:  |||  |||||  |||||  |||||  |||||  |||||  |||||
50 CysProGluValHisPro.....LeuProThrProValle 61
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
836 AGCCCT.....GCTAGAGAAAGCGCGCTATGGAG 805
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
61 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 77
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
804 TTGGCTCAAGCAGCTGCCAGCTGCAGGCGCTGGCTGGGCA..... 763
:|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
78 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 90
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
762 .....GCTGCTCAGGAGCCCGGAGGAT..... 739
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
90 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 107
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
738 .....GCCAGAGAGTGTCCGAGCAGCACCACGCTCCCTCGGG 703
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
107 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGly 123
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
702 GTGGCAGAGTTGTAGTGGCAGACAGCTT..... 673
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
124 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 140
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
672 ....CTCTGAGCGCTGCGCCATCGCCCTGGATCTCTCACTTGCTCT 627
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
140 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 156
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
626 AAGCTTTTAAAGGAAGCTCTGTGTAGACTCGAGGCGCGATATGTGG 577
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
157 .....ArgGlyLysValArgPhe 162
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
576 CGCAGACCGCTCGGAGCGGCCAGACCAACCCAGACCCACCTC 527
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
163 LeuMetLeuVal...GlyLysThrLeuCysValArgGlyGlySe 178
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
526 CGGACCGTAGCAGAGGTGA.....CCCTCTACAAGCATCAG. 487
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
178 rGlyGlySerGlyGlySerArgAlaProThrTyrArgAlaSerS 195
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
486 .....GAAACGACCTT.....TCCTCGGAGCAGGTGTGGAAGCT 451
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
195 erLeuProGlnSerPheLeuLysSerLeuGluGlnValArgLysIle 211
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
450 CAGAAAGATGCATGGGATCCTGTGAGCTGTGGCTCCCTCGCTGGAG 401
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
212 GlnGlyAsp.....GlyAlaAlaLeuGlnG 220
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
400 GAAGTGGTTCGAAGAGGCTGTGAGGCGCCCAAGGAGGAGCAGGACC 351
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
220 uLysLeuCysAlaThrTyrLysLeuCysHisProGluGluLeuValLeuL 237
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
350 TGTCCAGAAAGCTCCCGCAGGAGGATGAGAGCAAGTGGTCCCGAGTTG 301
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
237 euGlyHisSerLeu.....GlyIleProTrpAlaProLeu 248
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
300 TCCCGGTGCTGCCATCACTCCCTCCAGCAGAGGTCACGTCTCCCGAGAA 251
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||

249 SerSerCysProSerGlnAlaLeuGlnLeuAlaGly..... 260
250 TGTCCCTGTGCTGTGCTCTCTCCATCTGGGT 220
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
261 .....CysLeuSerGlnLeuHisSerGly 268

seq_name: US09680514.pep:US-09-680-514-35
seq_documentation_block:
; Sequence 35, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Giebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-680-514-35

alignment_scores:
    Quality: 93.00      Length: 17
    Ratio: 5.471        Gaps: 0
    Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
us-09-680-514-8 x US-09-680-514-35 ..

Align seg 1/1 to: US-09-680-514-35 from: 1 to: 17

523 TCCGGAGGTGGCTCTGCGGTTGTTCTGTTGGCGGCTCCGAGGCGGTG 572
|||||:  |||  |||  |||  |||  |||  |||  |||  |||  |||
1 SerGlyGlySerGlyGlySerGlyGlySerGlyGlySerGlyGly 17
573 T 573
17 g 17
```

```

seq_name: US09680514.pep:US-09-680-514-1

seq_documentation_block:
; Sequence 1, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-680-514-1

alignment_scores:
Quality: 89.50 Length: 258
Ratio: 0.814 Gaps: 14
Percent Similarity: 42.636 Percent Identity: 27.907

alignment_block:
us-09-680-514-8/rev x US-09-680-514-1
..
Align seg 1/1 to: US-09-680-514-1 from: 1 to: 328

886 TGTCCAGGTGGGACCACTCGGGGAGATCCCTTCAGGGCTGCAGG 837
|||||
29 CysProGluValHisPro.....LeuProThrProValLe 40
836 AGCCCT.....GCTAGAGAAAGCGGCTATGGAG 805
|||||
40 uLeuProAlaValAspPheSerLeuGly.GluTrpLysThrGlnMetGlu 56
804 TTGGCTCAAGCAGCTCCAGCTGCAGGGCTGCTGGGCA..... 763
|||||
57 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 69
762 .....GCTGCTCAGGGAGCCCGAGGAT..... 739
|||||

```

```

69 uLeuLeuGluGlyValMetAlaAlaAraGlyGlnLeuGlyProThrCysL 86
738 .....GCCAGAGAGTGTCCGAGCAGCAGCAGCTCCTCGG 703
86 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 102
702 GTGGCACAGCTGTAGTGGGCACAGCTT..... 673
103 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProGlnGlyArgThrTh 119
672 ....CTCCTGGAGCGCTCGGCATCGCCCTGCATCTTCTCCTCCTGCT 627
119 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 135
626 AAGCTTTTAAAGGAAGCTCTGTGTAGACTCGAGGCGCATATGTTGG 577
136 .....ArgGlyLysValArgPhe 141
576 GCGACGACCGCTCGGAGCGCC.....ACCAGAACCCAGC 539
142 LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProThrTy 158
538 CAGAGCCACCTCCGAGCCGTAGCGAGAGGGTGGACCCCTCCTACAAGCATC 489
158 rArgAlaSerSerLeuPro.....G 165
488 AGGAAACGCACCTTTCCTCG...GAGCAGGTGTGGAGCTCAGGAAGAT 442
165 InSerPheLeuLysSerLeuGlnValArgLysIleGlnGlyAsp 181
441 GGCATTGGGATCCTGTGAGCTGTGCTCCTCGCTGTGGAGGAGCTGGG 392
182 .....GlyAlaAlaLeuGlnGlyLysLeuCy 190
391 TTCCAGAGAGCTCTGACGGGCCCCAAGGAGGAGAGGACCTGTCCAGAA 342
190 sAlaThrTyrLysLeuCysHisProGluGluLeuValLeuGlyHis 207
341 AGCTGCCCGAGGAGGATGACAGGCAAGTGGTCCAGTGTCCCGGTC 292
207 erLeu.....GlyIleProTrpAlaProLeuSerSerCys 218
291 TGCCATCACCCTCCAGCAGAGGGTCACTGCTCCAGAAATGCTGTGTG 242
219 ProSerGlnAlaLeuGlnLeuAlaGly.....Cy 228
241 CCTTGGTCTCCTCATCTGGGT 220
228 sLeuSerGlnLeuHisSerGly 235

seq_name: US09680514.pep:US-09-680-514-5

seq_documentation_block:
; Sequence 5, Application US/09680514
; GENERAL INFORMATION:
; APPLICANT: Yokoi, Haruhiko
; Shiotsu, Yukimasa
; Konishi, Noboru
; TITLE OF INVENTION: NOVEL POLYPEPTIDES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 North Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

```

; APPLICATION NUMBER: US/09/680,514
; FILING DATE: 06-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/765,337
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP P.HEI.7-102625
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 249-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 5:
;     LENGTH: 349 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-680-514-5

alignment_scores:
    Quality: 89.50      Length: 258
    Ratio: 0.814        Gaps: 14
    Percent Similarity: 42.636    Percent Identity: 27.907

alignment_block:
us-09-680-514-8/rev x US-09-680-514-5 ..

Align seg 1/1 to: US-09-680-514-5 from: 1 to: 349

886 TGTCCAGGTGGGACCACTCGGGGAGATCCCTCCAGGGGCTGCAGG 837
|||||:|||||
50 CysProGluValHisPro.....LeuProThrProValle 61
836 AGCCCTC.....GGTAGGAAAGCGCGCTATGGAG 805
|||||
61 uLeuProAlaValAspPheSerLeuGly.GlutrPlyThrGlnMetGlu 77
|||||
804 TTGGCTCAGCAGCTGCCAGCTCGAGGCGCTGGTGGGCA..... 763
|||||
78 GluThrLysAla.....GlnAspIleLeuGlyAlaValThrLe 90
|||||
762 .....GCTGCTCAGGGAGGCCAGGGAT..... 739
|||||
90 uLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGlyProThrCysL 107
|||||
738 .....GCCCAGAGAGTGTCCGAGCAGCAGCTCCCTCGGG 703
|||||
107 euSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuGly 123
|||||
702 GTGGCAGAGCTTGTAGTGGCAGACAGCTT..... 673
|||||
124 AlaLeuGlnSerLeuLeuGlyThrGlnLeuProProGlnGlyArgThrTh 140
|||||
672 ....CTCTGAGCGCTGCGCATCGCCCTGGATCTCTCCTCCTGCTCT 627
|||||
140 rAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeu. 156
|||||
626 AAGCTTTTAAAGAGAGCTCTGTGTAGACTCGAGCGCGATATGTTGG 577
|||||
157 .....ArgGlyLysValArgPhe 162
|||||
576 GCGACGACCGCTCCGAGCGGC.....ACCAAGACACCGC 539
|||||
163 LeuMetLeuValGlyGlySerThrLeuCysValArgAlaProThrTh 179
|||||
538 CAGAGCCACCTCGGACCTACGAGAGGCTGGACCTCTCTACAAGCATC 489
|||||

```

```

179 rArgAlaSerSerLeuPro.....G 186
488 AGGAAACGCACCTTCTCTCG...GAGCAGGTGTGGAGCTCAGGAAGAT 442
|||||
186 lnSerPheLeuLeuLysSerLeuGluGlnValArgLysIleGlnGlyAsp 202
441 GGCATTGGGATCCTTGTGAGCTGTGGTCTCTCCCTGTGGAGGAAGCTGGG 392
|||||
203 .....GlyAlaLeuGlnGluLysLeuCy 211
391 TTCCAGGAGGCTCTCGAGGCCCCAAGGAGGAGACGACCTGTCCAGAA 342
|||||
211 sAlaThrTyLysLeuCysHisProGluGluLeuValLeuGlyHis 228
341 AGCTGCCCGGAGGAGGTGAGAGCAAGTGGTCCCAAGTTGTCCTCCCGTGC 292
|||||
228 erLeu.....GlyIleProTrpAlaProLeuSerSerCys 239
291 TGCCATCACTCCCTCCAGCAGAGAGGTCTACTGCTCCAGAAATGTCTGTG 242
|||||
240 ProSerGlnAlaLeuGlnLeuAlaGly.....Cy 249
241 CCTTGGTCTCTCCATCTGGGT 220
|||||
249 sLeuSerGlnLeuHisSerGly 256

```